

# FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCTCTAGAGATCCCTCGACCTCGA  
CCCACCGTCCGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTCGCTTCCCG  
CAGCGCTACCCGCCATGCGCCTGCGCGCCGGCCGCTGGGCTCCTGCGCTTCTGCTG  
CTGCTGCCGCCGGCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCGTGCGGGGGCT  
GGTGGACAAGTTAACCAAGGGGATGGTGACACCGCAAAGAAGAAACTTTGGCGCGGGAAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCTGCTGGAGATC  
CTGGAGGGGCTGTGCGAGAGCAGCAGTCAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCTGGCTGAGCTGAAGAGCGAATATCTGACTTATCGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGAACCTACGGTCCCGACTGCTCGCATGC  
CAGGGCGGATCCCAAGAGGCCCTGCGAGGGAAATGGCCACTGCGAGGAGATGGGAGCAGACA  
GGGGCAGGGTCTGGCTGCCACATGGGGTACCAAGGGCCGCTGTGACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGAACAGAACCCACAGCATCTGCACAGCTGTGACGAGTCC  
TGCAAGACGTGCTCGGGCTGACCAACAGAGACTGCGGGAGTGTGAAGTGGCTGGGTGCT  
GGACGAGGGCGCTGTGTTGAGTGTGGACGAGTGTGCGGCCAGCCCTCTGCGAGCGCTG  
CGCAGTTCTGTAAGAACCCAACGGCTCTAACCGTGCAGAGAGTGTGACTCCAGCTGTG  
GGCTGCACAGGGGAAGGCCAACGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGAGGAAAACG  
AAAACGTACAATACTCCAGGGAGCTACGCTGTGTTGCTCTGACGGCTTCGAAGAACG  
GAAGATGCTGTGTCGCCCGAGAGGCTGAAGCCACAGAACAGGAGAACGCCGACACAGCT  
GCCCTCCCGCAAGACCTGTAATGTGCCGACTTACCTTAAATTATTCAGAAGGATGTCC  
CGTGGAAATGTGCCCTGAGGATGCCGTCTCTGCAGTGGACAGCGGGGGAGGGCTGC  
CTGCTCTAACGGTGATTCTCATTTGTCCCTAAACAGCTGCATTCTTGGTTGTTCTTA  
AACAGACTGTATATTTGATACAGTTCTTGTAAATAAAATTGACCATTTGAGGTAAATCAGG  
AGGAAAAAAAGGGCGCCGCGACTCTAGAGTCACCTGAGAACAGCAATAGCA  
TTGGCCGCATGCCAACCTGTGTTATTGCACTTATAATGGTTACAATAAGCAATAGCA  
TCACAAATTTCACAAATAAGCATTTCACTGCAATTCTAGTTGTGGTTGTCACAAACTC  
ATCAATGTATCTTATCATGTCGGATCGGAATTAAATTGGCGCAGCACCATGGCTGAAAT  
AACCTCTGAAAGAGGAACCTGTGTTAGGTACCTCTGAGGGGAAAGAACAGCTGTGAAATG  
TGTGTCAGTTAGGGTGTGAAAGTCCCAGGCTCCCAAGCAGGAGAACAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTT

## FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRAALGLLPLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESEIRL  
LEILEGLCESSDFECNQMLEAQEEHILEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPCLACQGGSQRPCSG  
NGHCSGDGSRQGDGSCRCHMGYQGPLCTCDMGYFSSLRNETHSICTACDESCTKTCSGLTNRDCGECEVGWVLDE  
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSVGCTGEGPGNKECISGYAREHGQCADVDECSLAEKT  
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAETEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

## FIGURE 3

CAGGTCCAAC TGCA CCTCGG TTCTATCGATTGAAT TCCC CGGG GAT CCTCTAGAGA TCCCTC  
GACCTCGACCCAC CGCGTCCGCAGCGGGAGGCACGCCAGCGCTAAACGGAA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGCCAGGGTGCAGGTGCG  
GCACGAGGAGTTTCCCGGAGCGCAGGAGGCTCTGAGCGAC **ATGGCCGGAGGAGCGCCTC**  
CCTGGCCGGCCGCTCTGGAGCATCCTCTGAGCTGGCAGTGCCTGAGGAGCTGCAGGGAGGC  
CGGGCCGCCAGGAGGAGCGCTGACCTATGATCGATGCTCACAGGCAAGAGTACTCA  
TAGGATTGAGAAGAGATATCTGATTGTTAGAGGGAAAATGGCACCTTTACACATGAT  
TTCAGAAAAGCCAAACAGAGAATGCCAGCTATTCTGTCATATCCATTCCATGAATTTTAC  
CTGGCAAGCTGCAGGGCAGGCAAGAATCTCTATGAAATTCTGCTGGCCTCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCATGTCCCTGCTGGAACAGTGCCTCACAGGCA  
TCAGTTGTTCAAGTTGGTTCCCATGTCCTGGAAAACAGGATGGGTGGCAGCATTTGAAGT  
GGATGTGATTGTTAGATTGAACTTGAGGCAACACCATTCTCCAAAACACTC  
TCTTAAACATGTCACAAAGCTGAGTGCCTGATGGGTTCCAGGGACCTCAGTGAGAAAGCCCTTG  
GAAAGACGCATCTGCAGTGTCTGATGGGTTCCAGGGACCTCAGTGAGAAAGCCCTTG  
TACCCACAGATGATGAAATGGGACTTTGTGACTCTCTGATCTGCCCACCTG  
GATTCTATGGAGTGAACTGTGAAACAGCAAATGCTCACCCACCTGCTTAATGGAGGAGC  
TGTGTTCTACCTGGAAAATGTAATTGCCCCCAGGACTAGAGGGAGACAGTGTGAAATCAG  
CAAATGCCACAAACCCCTGCGAAATGGAGGTTAAATGCAATTGGTAAAGCAAATGTAAGTGT  
CCAAAGGTTACAGGGAGACCTCTGTCAAAGCTGTCGGAGCTGGCTGTGACAT  
GGAACCTGCGCATGAACCCAAACATGCCAATGTCAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCAGCCTACATGCCCTGAGGCCAGCAGGCCAGCTAGGCAGC  
ACAGCCCTTCAAAAAGGGCGAGGAGCGCCGGATCACCTGAATCCAATTACATCTGG  
**TGAACCTCGACATCTGAAACGTTTAAGTTACACCAAGTTCATAGCCTTGTGTTAACCTTCA**  
TGTGTTGAATGTTCAAAATGTTCACTTAAACTGAGGACTTCTCTTTAAGTTCTAAGTACGCTGTAG  
TCATTATAATCACTGAGCTGATTTACTCTCTTTAAGTTCTAAGTACGCTGTAG  
CATGATGGTATAGATTCTTGTGTTCAAGTGTGCTTGGGAGCAGATTATATTATGTC  
TCAGGTTAAAATTCTTCACTGAGCTGAGTTCAAGTGTGCTTGGGAGAATTTCTCAA  
ATTACATGATTATGGTGTCTGGGGCAGGGAAACATCAGAAAGGTTAATTGGGAAAAATGCG  
TTGGATGGTGCAGTTAATGTTGAAGTTCAAGCATTTCAGATTTCAGATTTCTCAGATATTAGAT  
GTTGTTACATTTTAAAATTGCTCTTAATTTTAAACTCTAACATATATTGGC  
TTACCAATTATTCAAGAGATTCACTGAGTTAAACAAAAAAATTACACTGTTGAGTGGCATT  
AAACAAATAATATAATTCTAAACACAATGAATAGGGAAATATAATGTTAG  
TGGCTTGAGCAATAATATAATTGTAACAAAACACAGCTTACCTAATAAACATT  
ACTGTTTGTATGATAAAAATAAGGTGCTGCTTTAGTTTTGGAAAAAAA  
AAAAAAAAAAAAAAAGGGCGGCCCGACTCTAGAGTCGACCTGAGCTGGC  
CGCCATGGCCCAACTGTTATGAGCTTAAATG

## **FIGURE 4**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094  
><subunit 1 of 1, 379 aa, 0 stop  
><MW: 41528, pI: 7.97, NX(S/T): 2  
MARRSAFPAAALWLWSILLCLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQRMPAIPVNIIHSMNFTWQAAGQAELYFVFLSLRSLDKGIMADPTVNPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC  
RNNGFCNERRICECPDGFHGPCHCEKALCTPRCMNGGLCVPGFCICPPGFYGVNCDKANCST  
TCFNGGTCFYPGKICCPPGLEQEQCEISKCPQPCRNGGKCIKGSKCKCSKGYQGDLCSPVC  
EPGCAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP  
PESNYIW

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## FIGURE 5

CGGACGCGTGGCGTCCGGCGTCGAGAGCCAGGAGGGGGAGGCGCGGGGCCAGCCCTGGG  
CCCCAGCCCCACACCTTCAACAGGGCCAGGAGGCCAATGTCGATGTCACCTGGGCTAC  
TGCCTGCTGCGCTGGCTGCCACTTGGCTCTGGGTGCCAGCAGGGCTGTGGGCCGG  
GAGCTAGCACCGGTCTGCACACTGCGGGCATCCGGACCGCGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGGCGGTGCCAGGACTGTGCCCTACCTGGGCCATCT  
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCGACTGTCGACTGATCTGGGACTTC  
TGCCCTCGGCGTGCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTCTATCTA  
TCCAGTCTGGGAACGTAACGGGAACTGTAAACCGTTGCACCTGCCAGGAGAACAGGCACTG  
GGCATGGTGGATTCCAGACATGATCAAAGCCATCAACAGGCCAACTATGGCTGGCAGGTGG  
GAACACAGGCCCTCTGGGCATGACCTGGATGAGGGCATTCGCTACGCCCTGGCACCA  
TCCAGCTTCCCTCGGTCTGAACATGATGAAATTATACAGTGTGTAACCCAGGGAG  
GTGCTTCCCACAGGCCCTCGAGGCCCTGTAGAAAGTGGCCAACCTGATTCTATGAGGCTCTTGA  
CCAAGGCACTGTGAGGCTCTGGCCCTTCACAGCACGGTGTGATCGATCTGTGCT  
AACTCCATTCTCTGGACACATGACCCCTGTCTGTGCCCCAGAACCTGCTGTCTTGAC  
ACCCACCGACAGGCCCTGCGCGTGGCGCTGATGGTGTGCTGGTGTCTGGCTCG  
CTGGCCCCCTGTATGATGCAAGCCGAGGATGGGTGGGGCAAGGCCAGGCCACTGCC  
CACTGCCCCAACAGCTATGTTAAACATGACATCACCAGGTCACTCTGTCTACGCCCT  
CGGCTCCAACGACAAGGAGATCTGAAGGGAGCTGTGGAGAATGGCCCTGTCCAAGGCCCTCA  
TGGAGGTGATGAGGACTCTCTCTATACAAAGGGAGGACTCATACGCCAACGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACCGCGGCCATGGGACCCACTCAGTCAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAGGACGCTCAATACTGAGCTGCGGCCAACTCTGGGGCC  
CAGGCTGGGGCGAGAGGGCCACTTCCGATCGCAGGCCGCTGGCATGGGACATGGGTCA  
AGCTTCTGTGCTGGCGTCTGGGCCCGTGGGATCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG  
CGGGCAGGCTGACCCAGCTCGCCCGACAGGCCGGGGCGCAGGCCGGGCCAGGGCGCTTAAT  
CCCCGGCGGGGTCTCCCTGACCGAGCGCCCCCTGGGAGCCGCCAGGGCAGGCGAGACTGGCG  
GAGCCCCCAGACCTCCAGTGGGACGGGCCAGGGCTGCCCTGGGAAGAGCACAGCTGCAG  
ATCCCAAGGCTCTGGGCCCTCAAGACTACCAAAAGGCCAGGACACCTCAAGTCTCCAGC  
CCCAATACCCCCACCCCAATCCGATTCTTTTTTTTACAGGGCTTGTGCTCCG  
TTGCCCAAGGTTGAGTGCAGTGGCCCATCAGGCTCACTGTAACCTCCGACTCTGGGTTCA  
AGTGAACCCCTCCACCTCAGCCTCTCAAGTACGCTGGACTACAGGTGCAACACCAACCTGGC  
TAATTTTGATTTTGTAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC  
CTGGGCTCAAGGGTCCACCTGCCCTGCCCTCAAGTGTGGATTGCAAGGCATGAGCC  
ACTGCACCCAGGCCGTATTTTATTCAGATATTATTTCTTCACTGTTTT  
TAAACCAAAGTATTGATAAAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLLCCRGRADDC
ALPYLGAICYCDLFCNRTVSdccPdFWDFCLGVPPPFppIQCmHGGRIYpVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
```

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTCGTTGTCCTCAAATCCA  
ATTCTCTGGGACACATNACGCCCTGCCTTNGCCCCAGAACCTGCTGTTGTACACCCAC  
CAGCAGCAGGGCTGCCCGGNTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCGCCAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGCGCCAGGCCACTGCCCACACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGGAGATCATGAAGGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTTCTTCTTACAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG  
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

## FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGG  
GAGCAGTGCTGGACCGCGCAGTCGGCAGTTGGCCTCTGACCGTCAGCAAAGGCTG  
CAGCTTGAACTGCGTGGA**TG**ACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCAGACTGTGCAACGCCAGCGGGGCCATGCCTGCAGCCGGCTGCCATCCTT  
GCGCTGCTCCCTGCACTCGCCTGCTGCTCTGGGACCCGGCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGGTGCCTCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCAGTGGGAGCCTGTCCTGAGGCACATCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCTCACCTGACCCCTCCATGGCCCTCCAGGACTCCCACCGCAGA  
TCAGCTCTAGTGACACAGATCCGCTGCAGATGGCCCTCCAAACCCCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCACCCCTAACCCCTGCTCAGGCACCTCTTCCCCAGGAAGCCTT  
CCCTGCCACCCATCTATGACTTGGAGCCAGGTCTGGTCCGTGGTCCCCGACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCAG**TAA**AGGCTGAGATGAAGTGGACTGAGTAGAACTGG  
GGACAAGAGTCGACGTGAGTCCCTGGGAGTCTCCAGAGATGGGCCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
**AATAAACACCTGTTGGATAAGCCAAAAAA**

## **FIGURE 9**

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSDT  
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVSPAPSRGQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## FIGURE 10

CCACACGCGTCCGAACCTCTCCAGCG**TGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT**  
GCTTACAGCTGCTGATTCTCTGCTGTCAGAACACTCAGTACGTGAGGGACCAGGGGCCATGACC  
GACCAAGCTGAGCAGGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTCAGGTACCCGGGCGTCGATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCGGGGTTGCGATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAAACAAGAGGGCAAGCTCATCGGGAAAGCCCAGCGGGAAAGAGCAAAGACTG  
CGTGTTCACGGAGATCGTGGAGAACAAACTATACGGCCTTCCAGAACGCCCGGCACGAGG  
GCTGGTTCATGGCCTTCACCGGGCAGGGGGCCCGCCAGGCTCCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGTGGCCTTCCCCAACACGC  
CGAGAACAGCAGAGCAGTTGAGTTTGTGGGCTCCGCCAACCGCCGACCAAGCGCACAC  
GGCGGCCAGCCCTCACG**TAGT**CTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCCCTCC  
CACCCCTTCCCTCTTAATCAAGGACTGGCTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCTGAGGGCCCGAAGCATTGGAGCCCCAGCTGGGAAGGGGAGGCCAGGGTG  
CCCCAGGGGGCGCTGGCACAGTGCCCCCTTCCGGACGGTGGCAGGCCCTGGAGAGGAAC  
GAGTGTCAACCTGATCTCAGGCCACCAGCCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC  
CCCTGAAAGGTCAAGCGACTGAAGGCCCTGCAAGACAACCGTCTGGAGGGCTGTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTAGCCCCCAAACCTCTGGCTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCAGCCC  
CGGAATAAAACCATTTCCTGC

## **FIGURE 11**

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPGSKDCVFTIEVLENNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTGCCATCACCTGTTGCCAGTGGAAAAATTCTCCCTGTTGAATTTCAGACATGGAG  
GACAGCACAAAGAGGGCAACACAGGCTGATAAGACCAAGAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCACAGAACCCCATCCAGT  
CATTTGATTTGCTGTTTATTTTCTTTTCTTTTCTTTCCACACATTGTATTAT  
TTCGGTACTTCAGAAATGGCCCTACAGACCAAAAGTGGCCAGCCATGGGCTTTTCT  
GAAGTCTGGCTATCATTCCTGGGGCTACTCACAGGTGTCACAAACTCCCTGGCTGCC  
CTAGTGTGCGGCTCGGACAGGAACCTTGCTACTGTATAAGCGAAGCTTGACCTCAGTG  
CCTCTGGGATCCCGGAGGGCCTACCGTACTCTACCTCCACAAACACAAATTAAATAATGC  
TGGATTTCCTGCAGAACTGCAATGTACAGTGGTGCACACGGTACCTGTATGGCAACC  
AACTGGACGAATCCCCATGAACCTTCCAAGAATGTCAAGAGTTCTCATTGCAAGAAAAC  
AATATTCAAGACCATTTACGGGCTGCTCTTGCCAGCTCTGAAGCTTGAAAGAGCTGCACCT  
GGATGACAACCTCATATCCACAGTGGGGTGAAGACGGGCTCCGGGAGGCTATTAGCC  
TCAAATTGTTTGTCTAAGAATACCTGGAGCTGTGGCTTGTGGCTTCTGTGGAC  
TTGCAAGAGCTGAGATGGATAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA  
TCTCACGAGCTGGGATCTTATGGACGGGAAACCTCTGACCCAACAGGTATCGCC  
AGGCACCTTCAGGACATCTACCAAGCTCAAGGAAATTCTCAATTGTACGTAATTCTGCTGCC  
CACCCCTCTCCGATCTCCAGGTACGCATCTGATCAGCTCTATTGCAAGGACAACCAAGAT  
AAACACAACTTCCCTTGACAGCCTTCTCAAATCTGCTGAAGCTGGAACGGCTGGATATATCCA  
ACACACCAACTGGGATGCTGACTCAAGTGGGGTTTGATAATCTCTCCAAACCTGCAAGGAGCTC  
ACTGCTCGAATAACCCCTTGTTGTGACTGCACTTAAATGGGTACAGAATGGCTCAA  
ATATATCCCTCATCTCTCACGTGGGGTTCATGTGCAAGGTCTGAACAAGTCGGG  
GGATGGCGTCAAGGAATTAAATGATCTTGTCTCTGCCACAGGACCCCCGGCCCTG  
CCTCTCTCACCCAGCCCCAAGCTACAGCTCTCCGACACTCAGCCTCCACCCCTCTAT  
TCCAAACCTAGCAGAAAGCTACAGCCTCCAACCTCTACACACATCGAAACTTCCACGATT  
CTGACTGGGATGGAGAGAAAGGTGACCCACCTATTCTGAAACGGATCCAGCTCTCTATC  
CATTTGTGAATGATACATTCAAGTCAGCTGGCTCTCTCCTTACCGTGATGGCATA  
CAAACATCACATGGTGAAGGCAACAGTTAGTAGGGGATCGTCAGAGCGCATAG  
TCAGCGGTGAGAAGAACACCTGAGCCCTGTTAACCTAGAGCCCCGATCCACCTATCGGATT  
TGTTTAGTGGCACTGGATGCTTTAACCTACCGCGGGTAGAAGACACCATTTGTTCAGAGGC  
CACCCACCATGCTCTCTATCGAACACCGGCAAGCAACAGCGTCCAGGCATGAGCAGAGA  
CGTCCCACAGCATGGGCTCCCCCTTCTGCTGGGGGTTGATCGGGGGCGGGTGATATT  
GTGCTGGTGGCTTGCTCAGCTCTTTGCTGGCATATGCACAAAAGGGGCGTACACCTC  
CCAGAAGTGAATACACCGGGCCGGCGGAAGATGATTATTGCGAGGCAAGGACCAAGA  
AGGACAACCTCATCTGGAGATGACAGAACACAGTTTCAGATCGTCTCTAAATAACGAT  
CAAACCTTAAAGGGAGATTTCAGACTGCGCCATTACACCCAAATGGGGCATTAAATT  
CACAGACTGCCCCATACCCCAACACATGCGATACTGCAACAGCAGCGTGGCAGACCTGGAGC  
ACTGCCCCATACGTGCAAGCCAGGGCTATCAAGGGGCAACATTAGACCTTGTGAGAA  
CACACTCGTGTGTCACATAAAGACACGCAGATTACATTGATAAAATGTTACACAGATGCT  
TTGTGCAATTGAAACTCTGTAATTATACGGTGTACTATATAATGGGATTTAAAAAAGTG  
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACTCTTGCTTTAATCTT

## FIGURE 13

MGLQTTKWPSPHGAFFLKSWLIIISLGLYSQVS KLLACPSVCRCDRN FVYC NERSL TSVP LGIP  
EGVT VLYLHNNQINNAGF PAELHNVQSVHTVYLYGNQ LDEFPMNLPK NVRVLH LQENN IQT  
SRAA LQLL KLEELH LDDNS I STVG VEDG AFRE A ISLKL LFLSKN HLLS VPVGLP VD LQELR  
VDE NRIA V IS DMAF QN L TS LER LIVD GNLL TNKG IAE GTFS HLT K LKE F SIVRN SLSH PPD  
LPGT H LIR YLQDN QINH IPLT AFSN LRKL ER LDI SNNQ LRL M TQGVFDN LSNL KQ L TARN N  
PWF C DCSIK WVTEWL KYI PSS LNV RGF MCQG P E QVRGM A VRE LNMN LLS CPTT PGLP LFTP  
APSTASPTT QPPT L S I PNP SRS YTPP PT S K L P T I P DWD G RER VTP P I S E R I Q L S I H F V N D  
TSIQVSWLSLFTV MAYK L T WVKMGH S L VGG I V QER I VSG E K QHLS L V N L E P R S T Y R I C L V P L  
DAF NY R A V E D T I C S E A T T H A S Y L N N G S N T A S S H E Q T T S H S M G S P F L L A G L I G G A V I F V L V V L  
LSVFCW H M H K K G R Y T S Q K W K Y N R G R R K D D Y C E A G T K K D N S I L E M T E T S F Q I V S L N N D Q L L K G  
D F R L Q P I Y T P N G G I N Y T D C H I P N N M R Y C N S S V P D L E H C H T

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300, 522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

## FIGURE 15

MEKMLAGCFLLILQIVLPLAEARERSRGRSISRGRHARTHPTQTALESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLD1GPDVTRVGLLQYGSTVKNEFSLKTFFKRKSEVERAV  
KMRMRHLSTGTMGLAIQYALNIAFSEAEAGRPLRENVPRVIMIVTDGRPQDSVAEAAKARD  
TGILIFAIVGVGQDFNLTLSIGSEPHEDHFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVVCRCKQGYILNNSDQTTCR1QDLCAMEDHNCQLCVNVPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHEECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGPC  
EHECVNMEESYYCRCHRGYTLDPNGKTCRSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
NEDLKTCRSRVDYCLLSDHGCYSCVNMDRSFACQCPEGHVRLSDGKTCALKDSCALGDHGCE  
HSCVSSEDSFVCQCFCFGYILREDGKTCRRKDVCQAIIDHGCEHICVNNSDSTCECLEGFLA  
EDGKRCRKDVCKSTHGCEHICVNNGNSYICKCSEGFLAEDGRRKCTEGPIDLVFVID  
GSKSLGEENFEVVKQFVTGILDSLTISPKAARVGLLQYSTQVHTEFTLRFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQGEARPLSTRVPRRAIAVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKIAEEELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALEADSQRQDS  
PAGELPKTVQQPTESEPVTINIQDLLCSNFAVQHRYLFEEEDNLLRSTQKLSHSTKPGSPL  
EEKHDQCKCENLIMFQNLANEVEVRKLTQRLLEMTQRMEEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTCAGGGCTGGCTCCCGCGCACGCTCGGCCGCGCAGGCCG  
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGC  
**CATGATTTCCTCCCGGGGCCCTGGTACCCA**ACTTGCTCGGGTTTTGTTCTGGGCTGA  
GTGCCCTCGGCCCGCCCTCGGGGCCAGCTGCACTGCACCTGCCGCAACCGGTTGAG  
GCGGTGGAGGGAGGGAAAGTGGTCTTCAGCGTGGTACACCTTGACCGGGAGGTGCTTC  
ATCCCAGCCATGGGAGGTGCCCCTTGTGATGTTCTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTTGGTCACTCC  
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAACAAGGAAATCTAGGGCCACAGCATAAAACCT  
TAGAACTCAATGTACTGGTCTCCAGCTCCATCTGCCGCTCCAGGGTGTGCCCAT  
GTGGGGCAACGTGACCTGAGCTGCCAGCTCCAAGGAGTAAGCCCGTGTCAAATACCA  
GTGGGATCGGCAGCTTCCATCTTCAGACTTCTTGACACAGCATTAGATGTCACTCGTG  
GGTCTTAAGCCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCGAAGGCCAC  
AATGAGGTGGGACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGGTACCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC  
TCTGTACCAACGCCGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATAAGGAGGATGCC  
ATTGCTCCCCGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAAGAATGGGACCCCT  
TTCCTCTGTCACCTCGCACGAGCCCTCCGCCACCCATGGCCCTCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGCTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACAGAGAT  
GGGGCCCAACCTCAACCAATATCCCCATCCCTGGGGTTCTCCCTGGCTGAGCCG  
CATGGGTGCTGCGCTGTGATGGTGCCTGCCAGAGTCAGACTGGCTCTGGTAT**TGATGAC**  
CCCACCACTCATGGCTAAAGGATTGGGCTCTCTCCCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCTGACCCCTAGTACTCTGCCCAACCTCTC  
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGACTGAGGGCAGAGACTTCCAGTCAGTCACTGAGCTCCAGGC  
CCCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGTTAGGTTACTGGGAGAGGATAGGAAATCTC  
TTATTAACATGAAATATGTGTTGTTTCATTGCAAATTAAAGATAACATAA  
TGTTGATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA  
VVAGAVVGTILVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL  
SSVTSARALRPPHGPPRPGALTPPSLSSQALPSPLPTTDGAHPQPISIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCCTCCGCTCCTAGTGGTTTTCCACTTTG  
TTGAATTGTCCTATACTCAAATTGCAACAGACACCTGTCTCCAAATGCAAAATGTGA  
AATACGAATGAAATTGAGACCTGCTATTGCAACATGGGATTTCAGGAAATGGTGCACAA  
TTTGTGAAGAGTATAATGAAATTGAGCTTAACTCAGTCTGTGGCAGAAATGCTAATTG  
ACTAACACAGAAGGAAGTTATTGATGTGCTACCTGGCTTCAAGTCAGCAGTAACCA  
AGACAGGTTTATCACTAAATGATGGAACCTCTGTATAGAAAATGTGAATGCAAACCT  
TAGATAATGTCGTATAGCTGAAATATTAAATAAAACTTTAACAAAATCAGATCCATAAAA  
GAACCTGTGGCTTGTACAGAAGCTATAGAAATTCTGTGACAGATCTTCACCAACAGA  
TATAATTACATATAGAAATTAGCTGAATCATCTTCAACTAGGTTAACAGAACAAACA  
CTATCTCAGCAAGGACACCCCTTCAACTCAACTCTTACTGAATTGTAACCGTGAAT  
AATTGTTGCAAGGGATACATTGTAGITGGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTACAAAATCATGCACACTGTGCAACAGCTTAAAGGATATCCAGGCTTCC  
AAAAGACCACAGAGTTGTACAAATTCACCGGATATAGCTCTCAAAGTTTCTTTTGT  
TCATATAACATGAAACATATTCTCATCTCATATGAATATGGATGGAGACTACATAAATATT  
TCCAAGAGAGAAAAGTCATGATGAAATGGCAATGTGCAATTGATTTATATTATA  
AGAGTATTGGCTTTGCTTCATCATCTGACAACCTTCTATTGAAACCTCAAATTATGAT  
AATTCTGAAGAGGGAGGAAAGAGTCATATCTCAGTAAATTCTCAGTCTCAATGAGCTCAAACCC  
ACCCACATTATGAACTTGAAGAAAATAACATTACATTAAGTCATCGAAAGGTCAAGAGATA  
GGTATAGGAGTCTATGTGCAATTGGAAATTACTCACCTGTGACATTAAGGAGCTGCT  
TCAGAGGGCTGTGAGCTGACATACTCAAAATGAGACCCACACTCATGCCGTGTAATACCT  
GACACATTTCGAATTGATGTCTCTGGCTTCTCATGGTATTAAAGATTATAATTTC  
TTCAAGGAGTCATCAACTGAAATTATTCAGTGTGTTCTTGGCATATGCAATT  
ACCTCTGGTCTTCAGTGAATTCAAAGCACACAGGACAACATTCAACAAAATCTTGTG  
TAGGCTATTCTGTGCTGAACCTGTTTCTTGTGGGATCAATACAATACTAAAGCT  
TCTGTTCAATCTTGTGCGGAGCTGCAACTACTCTTGTGCTTTGATGGATGTGC  
ATTGAAAGGATCATCTCATCTCATGGTGTGGGTGTCATCTACAAACAGGAGTTTGCA  
CAAGAATTTTATATCTTGGCATCTAACGGCCAGCGTGGTAGTTGGATTTCGGCAGCAC  
TAGGATACAGATATTATGGCACAACAAAGTATGGCTTAGCACCAGAAAACAACCTTATT  
TGGAGTTTATAGGACAGCAGTCCTAACTATTCTGTAACTCTTGTGCTTTGGAGTCAT  
CATATAACAAAGTTTCTGTCAACTGCGAGGTTGAAACAGGAAAGTTGCTTTGAGAAC  
TAAGGTCTGTGCAAGAGGAGGCCCGCTCGCTCTCTGTCTCTCGGACACCTGGATCTT  
GGGTTCTCATGGTGTGCGACATCAGTGGTTAACAGCTTACACTCTTCACAGTCAGCAATGC  
TTTCAGGGATGTTCATTTTATCTCTGTGTTTATCTAGAAAGATTCAAGAACAGT  
ATTACAGATTGTCAAAATGTCCCTGTGTTGGATGTTAACGTTAACATAGAGAACATG  
GTGATAATTACAAACTGCACAAAATAAAATCCAAGCTGTGGATGACCAATGTATAAAA  
TGACTCATCAAAATTATTAACACTAGAACAAAAGTATTAAATCAGTTTCT  
GTTTATGCTATAGGAACCTGAGATAAAGGAAATTATGATCATATAGATATACTATGT  
TTTCTATGTGAAATAGTCTGTCAAAATAGTATTGAGATATTGGAAAGTAATTGGTTT  
CTCAGGAGTGTATCACTGCACCCAAAGGAAGATTCTTAACACGAGAACAGTATGAA  
TGTCTGAAGGAAACACTGGCTGATATTCTGTGACTCGTGTGGCTTGGAAACTAGTCC  
CCTACACCTCGTAATGAGCTCATTACAGAAAGTGGACACATAAGGAATGAAGGGCGAGA  
ATATCAAACAGTGAAGAGGAATGATAAGATGTATTGATGAACTGTTTCTGTAGAC  
TAGCTGAGAAATTGTTGACATAAAATAAGAACACATTACCTTACATTGTGAA  
TTGTTCTGAACCTAAATGTCCACTAAACAACTTAGACTCTGTGCTAAATCTGTTCTT  
TTCTAAATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNNAKCEIRNGIEACYCNMGFSGNGVTCEDDNEC  
GNLTOSCGENANCNTTEGSYCMCVPGRSSSNQDRFITNDGTCIENVNANCHLDNCIAA  
NINKTLTKIRSIKEPVALLQEVYRNSVTDSLPTDIITYIEILAESSSLGYKNNTISAKDTL  
NSTLTLTEFVKTVNMFVQRDTFVWDKLSVNHRRTLTKLHMHTVEQATLRIQSFKTTEFDT  
NSTDIALKVFFFDPSYNMKH1HPHMNMDCDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLPKPNQYDNSEEERVISSVIVSVMSSNPFTLYELEKITFTLSHRKVTDRYRSLCAF  
WNYSPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGPGSIGKDYNILTRITQLG  
IIISLICLAICIFTFWFFFSEIYQSTRTTIHKNLCCSLFLAELVFLVGINTTNKLFCSITIAGL  
LHYFFLAFAWMCIEGHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVVLHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

### Signal peptide:

amino acids 1-19

### Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

### N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

### Glycosaminoglycan attachment site.

amino acids 49-53

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

### Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

### Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

### N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

### Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

## FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT  
TGGTCCCTTGTCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCAGTCAGTCAGCTCAAACCCACCCAC  
ATTATATGAACCTGAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTCTGGTCCTTCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTTGCCATATGCATTTTACCTTC  
TGGTCTTCAGTGAATTCAAAGCACCAGGA

## FIGURE 21

GCTCCCGAGCCAAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCG  
CTAACCGGAGGCCCTCCCTCCCGCAGATCGAACGCGCTGGCGGGGTCAACCCGGCTGGGA  
CAAGAAGCGCCGCGCTGCGTCCCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
GGTGTGAGTGGGTGTGCGGGGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
TGTCTTGGGACACTTACCCCTGG  
GGCGCGCCCGTCAAGAGCAGGGCGCTGGCTCCAGGATCTAGGGCCACGACCATCCAAACCC  
GGCACTCACAGCCCCGCGAGCGCATCCCGTGCGCCGCCAGCCTCCGCACCCCCATCGCCGG  
AGCTGCGCGAGAGAGCCCCAGGGAGGTGCCATGCGAGCGGGTGTGTGTGGTCCACGTATGG  
ATCTGGCCGCCCTGGCTGGCGTGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
CCACGTCACACTACGGCTGGGGGACCCCCATCCGCTGCGGACCTGTACACCTCGGGGGGGGG  
ACGGGCTCCTCAGCTGCTTCTGCGCATCGTGCGACGGCGTGTGGACTGCGCGGGGGGG  
CAGAGGG  
CGTGCACAGCGTGGGGTACCTCTGCGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
ACTCGGAGGAAGACTGTGCTTCGAGGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGGAAGCACCGCCCTCCCGTCTCCCTGAGCACTGCCAACACAGCGCAGCTGTACAAGAA  
CAGAGGGTTTCTTCACCTCTCATTTCTGCCCATGCTGCCATGTTCCAGGGGGGGGGGGGG  
AGGACCTCAGGGGCCACTTGGGAAATCTGACATGTTCTCTGCCCATGGAGACCGACAGCATG  
GACCCATTGGGCTTGTCAAGGACTGGAGGGCCGTGAGGAGGTCCAGCTTGGAGAAGTAACT  
GAGAGCATGGGACAGCTGCTGACTGCTGCCAGGGGGTGTGTGACCTCTGCAGCGTGGGGGGAGC  
TGCTTCTACAGAACAGTCTGAGTCCACGTTCTGTTAGCTTAACTCTAGGAAAGAAACATCTGAA  
GTTGTACATATTAGAGTTTCCATTGGCAGTGCAGTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCTGTAGCTTGGCCAGCTGCTGCCATGGGGCCCCCATCTGCTCCCTCGA  
GGTTGCTGGGACAGCTGCTGCACTGCTGAGTCTGCTGTTGAATACCTCCATCGATGGGGAAC  
TCACCTCTTGGAAAATTTCTTATGTCAAGCTGAAATTCTCTAATTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTAATTTCAGGAACAGGTGATCCAATCTGTA  
AAACAGCAGGTAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCAGGG  
ACCATTGGCCCTTCCCAAATCCCTCAGGGCAGAACACTGACTGGAGCAGGCATGGGGCCCC  
GCTTCAGGAGTAGGGGAAGCTGGAGCCCCACTCCAGGCCCTGGGACAACCTGGAGAATTCCCC  
CTGAGGGCAGTTCTGTCACTGGATGCTGCTGCTGAGAATAACTTGTGCTGTCACCTG  
TTCCATCTCCAGGCCAACAGCCCTGCGGCCACCTCACGCTCCCCATGGGATTTGGGGCT  
CCCAGGGCCCCCAGCTTATGTCAACCTGCACTTCTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCAATACTTGTGTTGGAAGCAGCGGGGGAGACCTAGAAC  
CTCTTATTCTTACATTATTATGCCCAAATTATTTATGTATGTAAAGTGTAGGTTG  
TTTGTATATTAAATGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVVHVWILAGLWLAVAGRPLAFSADAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHLRPLVSSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCAGAAGTCAAGGGCCCCCGGCCCTCGCTCTGCGCCGGGACCTCGACCTCTCA  
GAGCAGCGGCTGCCGCCGGAAAGATGGCGAGGAGGCCACCGCCTCTCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCATATGGTTCTGCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCTGCAAAACCCAA  
AGAAGACTGTTCCCTCCAGATTAGAGTGGAAAGAAACTGGTCGGAGTGTCTCTTGCTAC  
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCG  
GATCAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCTCATCG  
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCAGCAGTT  
CCATCATGTGAAGTACCCCTCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGAATCCAGCTCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACAAATGAATAACAAACTGGAACT  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAAATTCTGTGAAGGCCGCAATT  
TGGTGGATATCGCAGGTGTCTGGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCGTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAGGCTACTTTCAAAAGAACCTCTTCCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTGAAAATGTGCACTGGCTCACGCCGTAAATCCCAGCACTTGGAGG  
CCGGCGGGCGGATCAGGAGTCAGGAGTTCTAGACCACTGTCATGGCAATATGGTGAACCC  
CATCTCTACTAAAAACAAAAATTAGCTGGCATGGTGGCATGTGCCCTGCAGTCCAGCTGC  
TTGGGAGACAGGAGAACTGAAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAAATA  
ATAAAATACTGGTTTACCTGTAGAATTCTACAATAATAGCTTGATATT

## **FIGURE 24**

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIIRLLENPRLGSQST  
NSSYTMMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAAATGCTTTCAAGACGAGGAAGAGGAGGAGAAAAGAG  
AAAAGAAGAGGAAGATGTTGGCAACATTATTTAACATGCTCCACGCCGGACCTGGCAT  
CATGCTGTATTCCCTGCAAATACTGAAGAAGCATGGGATTAAATATTACTCTAAATAA  
ATGAATTAATCTCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA  
TTATATCATTAAGGAAATAGTAACCTTCTTCTCCAAATATGCACTGACATTGGACAAATG  
CAATTGTGCACTGGCACTTATTCTCAGTAAGAAAATCTTGTGGTTCTATGGCAATTCTA  
TTTGACAATGCAAGCATCTCTTATCAATCAGCTCTATTGAACCTACTAGCACTGACTG  
TGAATTCCTTCAAGGAAATCTTCTCAGTAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCTATGTGCTACTTGGCTTAGCTATCACTACACTAGTACAAGCTGTAGAAAAG  
TGGATTGTCACCGTTATGACCTGTGAATCAGGCCCTGGTTAACCCAGATCATTAT  
ATGGAAGCATCTACAGTGGATTGTAAATGATTTAGGCTTTAACITTCAGCCAGATTGCC  
AGCTAACACACAGATCTTCTCTCAGACATAAATATGCAAAAATATTGAAATACTCCACAG  
ACTTCCAGTAACACCTACTGGCTCTGGATTATCTCAAAACAAATTTATCTCAGTCACCAAT  
ATAATGTAAAAAGATGCCCTAGCTCCTTCTGTGTACCTAGAGGAAAACAAACTTACTGA  
ACTGCCGAAAATGCTGTGCGAACACTGCAACTAACAGAAACTCTATATTAAATCACAACT  
TGCCTTCTCACATTCTGAGGCCCTTATGGCCATACAAATCTTCTCAGCTTCATCTC  
AATTCAAATAGATTGCACTGATGCAACACTAAGTGGTTGATGCTTCAAAATCTAGAGAT  
TCTGATGATTGGGAAATCAATTATCAGAATCAGAACAGATGAACCTTAAGCTCTTATCA  
ATCTTCGAGCTGCGGTATAGCTGTAAACCTCACAGAAATACCAGATAACGCCCTGGTT  
GGAACCTGAAAATCTTAGAGAACACTCTTCTTACGATAACAGGCTTAAAGTACCCCATGT  
TGCCTCTCAAAAGTGTAAATCTCAAATTGGATCTAAATAAAATCTTATTAATAGAA  
TACGAAGGGGTGATTTTAGCAATGCTACACTTAAAAGAGTTGGGATAAAATAATGCTT  
GAGCTGATTTCATCGATAGTCTGCTGTGATAACTCGCAGAGATTTAAGAAAATAGAAC  
TACTAACACCCATGAGTTGCTTACATTCAACCCCAATGCACTTTTCAGACTCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGGCTGTACCTGTTGACTGCTCTG  
CCAAACCTCAAGGAAATCAGACATCACAGTAACCCCATCAGGTGTGACTGTGTCATCGTTG  
GATGACATGACAAAACCAACATTGATTCATGGAGGCCGATTCACTGTTTGCCTGGACC  
CACCTGAATTCCAAGGTCAAGATGTTCGGCAAGTGCAATTCAAGGGACATGATGAAAATTGT  
CTCCCTTCTTATAGCTCTGGAGACTTCTCTTCAATCTAAATGAGAAGCTGGGAGCTATGT  
TCTCCTTCTACTGTAGAGCTACTGCGAGAACACAGCGTGAAGATCTACTGGATAACACCTTCTG  
GTCAAAAACCTTGTGCTTAACCCCTGACAGACAAGTTCTATGTCATTCTGAGGGAAACACTA  
GATATAAAATGGCGTAACTCCAAAAGAAGGGGTTTATATCTTGTATAGCAACTAACCTGT  
TGGCGCTGACTTGAAGTCTGTATTGATCAAGTGGATGGAATTTCACAGAGATAACATG  
GCTCTTGAATATAAAAGAGATATTCAAGGCCATTCACTGTTTGTGCTGGAAAAGCA  
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA  
TGCTGCGAAAAGTGTGCAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATCTCCACCATCTATCAGAAAACAGAAAAAAA  
TGTGTAAATGTCAACCAACCAAGGTTGCACCCGTGATCAAAAGAGTATGAAAAGATAATAC  
CACAAACATTATGGCCTGCTTGGAGGCTTCTGGGGATTATTGGTGTGATATGCTTATCA  
GCTGCGCTTCTCCAGAAAATGAACACTGCGATGGTGGACACAGCTATGTGAGGAATTACTACAG  
AAAACCAACCTTGTGATTAGGTGAGCTTATCTCTCTGTAAATCTCTGGGAAGCAGGGAAA  
AGAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTACCAACAAATATGCTC  
AAAAACCCACCAAGGAAACCTACTCCAAAATGAAC

## **FIGURE 26**

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT  
FPARLPANTQILLLQTNNIAKIBYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTELPEKCLSELNSNLQELYINHNLLSTISPGAFIGLHNLLRLHNSNRQMINSKWFDA  
LENPNEILMIGENPIIRIKDMNFKEPLINLRSLVIAGINITEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVNVNLKFLDLNKPINRIRDGFDSNMLHLKELGINNNPELISIDS LAVDNLPD  
LRKIEATNPNRLSYIHPNAFFRLPKLESMLNSNALSAVHGTIESLNLKEISIHSNPIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVFSFHCRATAEPOPEIYWITPSGQKLLPNTLTDKFYVHSEGTLIDINGVTPKEGGGLYTC  
IATNLVGAIDLKSVMIKVDGSFPQDNNGSINIKIRDIQANSVLVSWKASSKILKSSVKWTAFV  
KTENSHAAQSARIPSDVKVYNLTHLNPESTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQE  
YEKNNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDDGHSYVRNYLQKPTFALGELYPPIN  
LWEAGKEKSTSLKVATVIGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

GC CGGG ACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTGAAACACGCCAAGAAGGAATCAATAGTGTGGACAGGGCTGGAACCTTAC  
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGAATTGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCGTCCCTCCATGTGTCCTCCTACAAAGTTGTTCTTA  
TGATAGTGTGCTTCATTCTGCCAGTATGTGTCCTAACGGGCTGTCCTGTTCTCCTCTGGG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAATACCTAGAGATCTCCCTCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG  
ACCTCCATCAACTGAGAGTTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTTGTCGACAATCGGATTCAAAG  
TGTGCAAAAAATGCCCTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGACATGGCGTCAATCATGAGACAGCCCAC  
AACGTGATCTGAAACGTCGTGTTGGATGAAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTGCGTGGTCACTATGGTGAATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG  
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA  
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTCTCCCATCCATTGTAACATTGAA  
ACTTTGATTTCACTGTTTTGAAATTGCCACTGCTGAACCTTAAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATGAAATTATTTTTT  
AATTAAAAGCAAATAAAAGCTTAACCTTGAAACCATGGGAAAAAAAAAAAAAAACAA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLQSFLMILCFHSASMCPKGCLCSSGGLNVTCSNANLKEIPRDL  
PPETVLLYLDQNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLDR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## **FIGURE 29**

ACCGAGCCGAGCGGACCGAAGGCGGCCGAGATGCGAGGTGAGCAAGAGGATGCTGGGGGG  
GGCTGAGGAGCATGCCAGGCCCCCTCTGGCGCTGTCGGAGGCCATCCTCTGCTGGTGCT  
GGCTCATGCTGTCAGGCTCGGCCAGGCGTCCGGCCCGCTGCGAGTGTCCGCCAGG  
ACCGCGCTGCTGCTGTCACCGCAAGTGTCTTGTGGACTGCCAGGAGCATCCCAACCGAG  
ACCGCCCTGCTGGACCTAGGAAGAACCGCATCAAACGCTAACCAAGGACGAGTTCGCCAG  
CTTCCCCACCTGGAGGAGCTGGAGCTCACCGAGAACATCGTGAGGCCGCTGGAGGCCGGC  
CTTCAACACCTCTTCAACCTCCGGACGCTGGCTCTCCGGACCAACGCCGTCAGGCT  
CCGCTAGGGCTTCACTGGCCTCAGAACCTGAGAACAGGAGACATCACCGAGAACAAAGAT  
CGTTATCTTCACTGGACTACATGTTCAAGGACCTGTACAAACCTCAAGTCACTGGAGGTTGGC  
ACAATGACCTCTGCTACATCTCACCGCCCTTCAGCGGCCAACAGCTGGAGCAGCTG  
ACGCTGGAGAACATGCAACCTGACCTTCAATCCCCACCGAGCGCTTCCACCTGCAACGCCG  
CATCGTCTGAGGCTCGGCACCTCAACATCAATGCCATCGGGACTACTCTTCAAGAGGC  
TGTAACCGACTCAAGGCTTGGAGATCTCCACTGGCCCTAATGGACACCATGACACCCAA  
TGCTCTACAGGCCCTCAACCTGAGCTCCCTGTCCATCACACATGCAATCTGACCGCTGTG  
CTACCTGGCCCTGGCCACACTGCTATCTGGCTTCAACTCTTCAACACCCATCA  
GCACCAATTGAGGGCTCCATGTTGATGAGCTGCTCGGCTGAGGGAGATCCAGCTGGTGGG  
GGGAGCTGGCCCTGGTGGAGCCCTATGCTTCCGGCCCTAACTACCTCGGCCGTGCTCAA  
TGCTCTGGCAACACGCTGACCAACACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG  
AGACACTCATCTGGACTTCAACCCGGCTGGCCCTGGCAGACTGTCGCTCTGTGGTGTCTGG  
CCGGCTGCGGGCTCAACTCAACCCGGCAGCAGGCCACGTGCGGCCACGCCAGTTGTCCA  
GGGCAAGGAGTCAAGGACTTCCCTGTGCTACTGCCAACACTTCACTCTGGCCGGCG  
CCGGCTACGGGGACCGCAAGGCCAGCGTGTGGTGTGGAGGGCCACCGTGTGCAAGT  
GTGTGCCGGGGCATGGCGACCCGCCGCCATCTCTGCTCTCACCCGAAACGACACCT  
GGTCTCAGGCAAGGACAATGGGGCTCACAGTCTTCCCTGTGCTACTGGCACTGGCT  
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCTACTGCCAACAGGGCCGGCAACGAC  
TCTCATGGCCGCCACTGCTGATGTGGCGACTACTGCCGACTGTGGCCCATCGACCAACAA  
GACCTTCCCTTCACTCCAACAGGGGGAGGGAGAGGCAACAGCACCGGCCACTG  
TGGCTTCCCTGGACATCAAGACCTCATCACGCCACCATGGGCTTCATCTCTTCC  
TGCGGCCCTGGCTCTTCTGCTGTGCTGTGTTCTGGAGGCCGGCAAGGCAACAC  
AAAGCACACATCGAGATCGAGATGTGCTGGCCAGGCGAGCATCGCTGCC  
ACCGGCCCGCAAGTCAACATGAAGATGATATGAGGGCGGGGGGGGGAGGGACCCCCG  
GGCGGCCGGAGGGGAGGGGCTGGCGGCCACTGTCTACTCTCAGTCTTCCACCTC  
CTCTCCACCTTCAACACAGTCTCTTCTCTCCCTGGCCCTGGGGGGGGGGAGGGACCCCC  
CCAGGCCCTCACCACTGCCCTCTTCAACAGGACCTCAGAGGCCAGACCTGGGACCCCC  
CCTACACAGGGGATTGAGACACTGGAGTGAAGGCCAGCAACCGGACAGCGGGAGAGTCA  
ATAATTCAATAAAAAGTACGAACATTCTCTGTAACTTGGTTCAATAATTATGATGTTT  
TATGAAAACCTGAAAATAAAAAAGGAAAAAAACTAAAAAAAGGAAAAAA

## FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVEPEGIPTETRLLDGLKNRIKTLNQDEFASFPHEEELNEENIVSAVEPGAFNNLFNLRTL  
GLRSNRKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDQDLYNLKSLEVGDNLDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHIVYLRFLNLSYNPISTIEGSMILHEL  
LRLQEIQLVGGQLAVVPEPYAFRGLNLYLRLVNVSQNLTTLEESVFHSGNLETLLIDSNPLA  
CDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL  
CTAAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCVLFLWLSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCCCACGGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTCGCCAGGCCAGCC  
AGGGAGCGGCCGGGAAGCGCGATGGGGGCCAGCCGCCCTCGCTCCTGCTCCTGCTCCTGC  
TGTTCGCCTGCTGGCTGGGCCGGGGCAACCTCTCCAGGACGACAGGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGCACCCTGGTCAAGTGCCAAGTGAAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTAGCTGGTTACCTCTACGCCACAGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCCTG  
GCGAAGCTGCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCAGGTT  
ATAAAATCTTCAATTACGGGAAAAAGACAGCCACCCCTAAACTGTCAGTCTTCTGGAGCAAG  
CCTGCAGCCGGCTCACCTGGAGAAAGGGTGAACAGAACACTCCACGGAGAACCAACCCGCA  
ACAGGAAGATCCAATGGTAAAACCTTCACTGTGCACTCGTGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATTGTGCTCTGTGAACCATGAATCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCTCGTGGGGCCAGAACGCTGCTACACTGTGAGGGTCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAACGGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTCCTAACAAAGAGTGAAGCTGACAGTGGCACCTACGGCTGACAGCACCA  
CAACATGGGAGCTACAAGGCCACTACACCCCTCAATGTTAACGACCCAGTCCGGTGCCT  
CTCCCTCAGCACCTACCAGCCATCATCGTGGGATCGTGGCTTCACTGCTTCTGCTG  
CTCATCATGCTCATCTCCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAGGCTCCGACGATGCTCCAGACGGGACACGGCCATCATCAATGCGAGAGGC  
GGCAGTCAGGGGGGACGACAAGAAGGAATATTCATTAGAGGCGCTGCCACTTCTGC  
GCCCCCAAGGGCCCTGTGGGACTGCTGGGGCGTCACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCGCTTGTCTCCAGCCACCCACCCCGTACAGAAATGTCTGC  
TTGGGTGCGGTTTGACTCGGTTGGAATGGGAGGGAGGGAGGGGGGGGGGGGGGG  
TTGCCCTCAGCCCTTCCGTGGCTTCTGCAATTGGTTATTATTATTTGTAAACATCC  
CAAATCAAATCTGTCCTCAGGCTGGAGGGAGGGCAGGCCCTGGGGTGAGAAAAGCAAAAACA  
AACAAAAAAACA

## **FIGURE 32**

MGAPAASLLLLLFFACCWPGGANLSQDDSQPWTSDETVVAGGTVVLCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSISISNVALADEGEYTCISIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSFTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKGSPVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCCACCCCCCAACCCCTTTCTTCTCCTTCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAAATTGTCGCTGTGGCAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGTTAAAATGCTGTTGGATTCTGTT  
GCTGGAGACGCTCTTTGTCGCTGAAACGTTACAGGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGGACCTACAGCTGAAAGGGCTTCAAGGAGAAGA  
AGTCTGAGCGTTTCACTGCCGACTTCCAGTTTACATTATTCTGCATGGCAATT  
CCTCACTCGACTTTCCCTAATGAGTCGTAACCTTTATAATGCGTTAGTTGCACATGG  
AAAACAAATGGCTTGCATGAAATCTGGGGGCTTTCTGGGCTGAGCTGGTGAAGAAGG  
CTGACATCACAAACAAGATCAAGTCTTCTGAAAGCAGACTTTCTGGGGCTGGACGA  
TCTGGAATATCTCAGGCTGATTAAATTATTACAGGATATAGACCCGGGGCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTATTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC  
GTGTTCCAGTATGTCGCCATCACCCACCTGCCACCTCCGGGTAACAGGGCTGAAAAGGCTGCC  
CTATGAGGAGTCTGGAGCAATTCCCTGTTATTGCGAGGATCTGCTAGAGGATAACCCCT  
GGGACTGCACTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC  
CTGATGCCGAGTCTGGCAAGGCCAACAGCTGCAAGGTAAGACCTCAATGAAC  
CACCGAACAGGACTTGTGCTTGGAAACAGGACTTGTGCTTCAAGACAAATGGCAAGAG  
GATCATGCCACACCAGGGCTGCTGCTCAAACGGAGGTAAAGATCCAGGCACTGGCAGAT  
AAAATCAGGACACAGCAGGATAGCAGGGTAGCTCAGGAAACAAACCCCTAGCTAAC  
GTTTACCCCTGCCCTGGGGCTGCACTGCCAACATCCAGGGTGGGTTAAAGATGAAAC  
TGAACAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAAGGA  
GCTTTCTACAGATAACAAAGATCCACAGCATCGAAATTCGCAACTTGTGGATTAAAGA  
ACCTCATTCTGTTGGATCTGGGCAAAATAACATCGCTACTGTAGAGAACAAACACTTCAAG  
AACCTTTGGACCTCAGGTGGCTATACTGGATAGCAATTACCTGGACAGCTGTCCGGGA  
GAAATTCTGGGGGCTGCAAACCTAGAGTACCTGAAACGTGGAGTACAACGCTATCCAGCTA  
TCTCTCCGGGCACTTCAATGCTGCACTGGGCAACTGGAGATCTCCATTCTCAAAACAAACCTG  
CTGAGGTCTCTGGCTGAGCTGGACCTGCTGGGGCTCTGCTCTAAACTCAGCCTGCAAA  
CAATTACTTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCATCCAGA  
TAGACCTCCAGGAACTCTGGGGATGCTCTGCAAAATTGTCGCTTCAACCGAGTGGGCA  
GAACGCTGGGGTCCGAAGTGTGATGAGGACCTCAAGTGTGAGACGCCGGTGAACCTT  
TAGAAAGGATTTCATGCTCCTCTCAAATGACGAGATCTGCCCTCAGTGTACGCTAGGATCT  
CGCCCACTGTAACCTGGCAGTAAACGACACTGGGTTGGCGGAGACCGGGAGCAGCACTCC  
AACTCTTACCTAGACACCAGGGGTCTCATCTGGTGTGGTCCGGGACTGCTGCTGGT  
GTTTGTACCTCCGGCTTACCGCTGGGATGCTGTGTTTACCTGGAGAACCGAAAGC  
GGTCCAAGAGACGAGATGCCAACTCTCCGGCTCCGGAGATAATTCCCTACAGACAGTCTG  
GACTCTCTCACTGGCACAAATGGGCTTACACGCGAGATGGGGCCACAGAGTGTATGACTG  
TGGCTCTCACTCGCTCTCAGACTAACGACCTGGGAAACCCCAATAGGGGAGGGCAGGGGAAGGG  
ATACATCCTTCCCACCGCAGGCCACCCGGGGCTGGAGGGGCGTGTACCAAATCCCGC  
CCATCAGCCTGGATGGCATAAGTAGATAAAATAACTGTGAGCTGCCACAAACGAAAGGGCT  
GACCCCTTACTTAGCTCCCTCTGGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA  
GCCAGCTGGCTTGGCTGAGGCCCTTGTGACAGAAAGGCCACAGCACCCCTGCTGGAG  
AACTGACAGTGCCCTGCCCTGGCCCCGGGGCTGTGGGGTTGGATGCCGCGTTCTATAC  
ATATATACATATACACATATAGAGAGATAGATACTATTTCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGGCTACGCGGGATGGGCACTTGCACGAGGATGAATGTAT  
TGTAATAAGTAACCTTGACTCTGAC

## FIGURE 34

MLLWILLLLETSLCFAAGNTGVDVCKEKI CSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTLRFLPNEFANTFVANSLHMMNGLHEVFGAFLGLQLVVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLLEVLIINDNLISTLPANVFQVPITHLDDRQ  
NRKLTKLPEVEYLQFPGIAETLLEDNLPWDCDTCDSLLKEWELENIPKNAI1GRVVCAPTRLQ  
GKDLNNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPPLPTFKTNQEDHATPGSAPNGGT  
1PGNNWQ1KIRPTAA1ATGSSRNKPLANSLCPGGCSCHDIPGSLKMNCCNRNVSSLADLKP  
KLSNVQELFLRDNKIH1RKSHPFDYKNL1LLDLGNNNIA1TVENNTFKNNLLDRWLIMYMDNSY  
LDTLSREKPAFLQNLNEYLNVEYNAIQLLPGFTFNAMPKRL1L1LNLLNRLSPLVDPVAGFVSL  
SKLSLHNMYFMYLPVAGVLDQLTSIIQ1DLHGNPWECSCT1VPFKQWAERLGSEVILMSDLKC  
ETPVNNFRKDFMLNSDE1CPLQYARISPTLTSHSKNTGLAETGTHNSYLDTSRVS1SVL  
VPGLL1VFTVSAFTVVGMLVFL1RNRKRSKRDANSASE1NSLQTVCDSSYWHNGPYNADG  
AHRVYDGGHSLSD

### Signal sequence:

amino acids 1-15

### Transmembrane domain:

amino acids 618-638

### N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

### Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577, 608-612, 657-661, 666-670, 693-697

#### N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349, 354-360, 465-471, 493-499, 598-604, 603-609

## Prokaryotic membrane lipoprotein lipid attachment site

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCCCGTGACCCGGCGCCAGCTGTGTTCTGACCCCCAGAATAACTCAGGGC  
TGCACCGGGCTCGCAGCGCTCGCACACATTCTCTGCGGCTAAGGAAACTGTGGC  
CGCTGGGCCGCGGGGGATTCTTGGCAGTGGGGGTCGTCGGAGCGAGGGCGGAGGG  
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGTGAACGGCCTCACAC  
AGCTCTGCGCTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGGG  
AGA**ATG**AGGCCGGCTTCGCCCCGTGCTCTCTGCGAGCGCTCTGGCCGGGGCTCGTACAGCTGC  
CGGCGAACACCCCACTGCCGACCGTGTGGCTGCTCGGCTCGGGGCTCGTACAGCTGC  
ACACCGCTACCATGAAGCGGAGCGGGCAGGAGCCGTCATCTGCGAGGTGGGGCGCTC  
AGCACCGTGCCTGCGGGCGCAGCTGCGCTGTGCTCGGCTCTGCGGGCAGGCCAGG  
GCCCGAGGGGCTCAAAGACTGCTGTTCTGGGTCGACTGGAGCGCAGGCCACTTCCACT  
GCACCCCTGGAGAACAGGCCATTGCGGGGTTCTCTGCTGCTCCGACCCGGCGTCTC  
GAAAGCGACACGCTGCAAGTGGGGAGGAGCCCAACGCTCTGCAACCGCGGGAGATGCGC  
GGTACTCTCAGGGCACCGGCTGGGTGCAAGCCCGAGGCTGAAAGAGATGCGATGCCACCTGC  
GCCAACAGGCTACCTGTGCAAGTACCAAGTTGAGGTCTGTGTCCTGCGCCGCCGG  
GCCGCCCTAATCTGAGCTATCGCGCCCTTCAGCTGCAACAGGCCCTCTGGACTTCAG  
TCACCTGGGACGGAGTGACTCGCGCTCGGGGACAGCTCCGATCTCAGTTACTTCGA  
TCGGCGACGAAATCGGCGCTGCTGGGAAACTCTCGGGGATGTGTTGTCCTGCCCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAAGAGCTCCCTAAGCCTAGCCTAGACGACTTGGGAGG  
CTTGCCCTGCAATGTCATGGGCTTCAGGCTGGGAGGAGCGCCGCTCTGTGACCA  
GTGGGGAAAGGACAGCCGACCCCTGGGGGACGGGGCTGCCACAGGCCGCCGGGACT  
GCAACCAGCCCCGTGCGCAGAGAACATGGCAATCAGGGTCGAGAGAACAGCTGGGAGAGAC  
ACCACTGTCCCTGAACAAAGAACATTCACTAACATCTTCCGAGATTCCTCGATGGGAT  
CACAGACGACGATGTCACCTCTCAAATGCTCCCTGAAGCCGAGTCAAAGGCCACTATACCC  
CCATCAGGGAGCGTGAATTCCAAGTTAATCTACGACTCTCTGCCACTCTCAGGCTT  
CGACTCTCTCTGCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGATCT  
TGACCATGACAGACTGGGGCTTGTCAAGCTCTGCTTACGAAAGGCCCTTCCAGCCA  
AGGAAGGAGTCTATGGGCCCCCGGGCTGGAGAGTGTACCTGAGCCGCTGCTTGGGCTC  
CAGTTCTGCACATTGACACAAACATGGGGTAAAGTCGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCCTTGTGGCGAGTCCCCTTGGCTCTAGTGATGTCAT**AGGAAACAGGGGA**  
CATGGGCACTCTGTGAACAGTTTCACTTTGATGAAACAGGGGACCCAAGGAACTTAC  
TTGTGTAACTGACAATTCTGAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAACACTGCACACTCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAA  
TGTTGATGACTGGGGACGGGTAGTGTGGGGAGAGATATTCTTATTGTTATTGGAGAA  
TTTGGAGAAGTGTGAACTTTCAAGACATTGAAACAAATAGAACACAAATATAATTACA  
TTAAAAAATAATTCTACCAAAATGGAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT  
ATTGGGTCGAAATCCAGGGAAAAAAATAAAAATAAAATTAAAGGATGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGEHPTADRGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAELRAVIALLRAAGPGPGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL  
SDTLQWVVEPQRSCATARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPG  
ASNLSSYRAPFQLHSAAALDFSPPGTEVSAALCRGQLPISVTCIADEGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGFFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA  
TSPVPVQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTSSATPQAFDSSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR  
KESMGPPGLESDEPAALGSSSAHCTNNGVKVGDCDLRDAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACCGTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCTCAGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATATCGCTTAAAGTGCCTCCGCCCTGCCGGCGCGTATC  
CCCCGGTACCTGGCCGCCCGCGCGGTGCGCGCGTGAAGAGGGAGCGCGCGGGAGCGA  
GCGCCGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGTGC  
GGGGCGTGTGCGCCGCCGCGCCGCGTGGGTGCAAAACCCCGAGCGTCTACGCTGCC**ATGA**  
GGGGCGCGAACCGCTGGGCCACTCTGCTGCTGCGTCCAGCTCCAGCTCTCGGG  
CAGCAGTCCCCAGAGAGACCTGTTCACTGTGGTGGCATTCTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTCTGGAGGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCCCGAAGAAAAGTAGTCGCTCTCAATTTCGATTAGACCTCGAGAGTGACAAAC  
CTGTGCCGTATGACTTGTGGATGTGTACAATGCCATGCCAGCGCATGGCC  
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGC  
TGATTTCTGTGCAACACAGCTGCCATGGCTCATGGCCATGTTCTCGCTGCTGAACCA  
AACGAAAGAGGGATCAGTATTGTGGAGGACTCTTGACAGACCTTCCGGCTTTTAAAC  
CCCCAACTGGCCAGACCGGGATTACCCCTGCAAGGAGTCACTTGTGTGGCACATTGAGCC  
CAAAGAGTCAGCTTATAAGATAAAAGTTGAGAAGTTGATGTGGAGGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGGGGGGAGTCACAGTGTAGAAGAATTGGAAA  
GTATTGTGGTGTAGTCCACCTGCGCAATTGTGCTGTAGAGAAATGAATTCTTATTCAGT  
TTTATCAGACTTAAAGTTAACTGCAGATGGGTTATTGGTCACTACATATTCAAGGCAAAA  
AAACTGCCTACAACTACAGAACAGCCGTGCAACACATCCCTGTAACCACGGGTTAAA  
ACCCACCGTGGCTGTGCAACAAAAGTAGTGAGACGGACGGGACTCTGGAGGGCAATTATT  
GTCAAGTGAATTGTATTAGCCGGCACTGTTATCACACCATCACTCGGATGGAGTTG  
CACGCCACAGTCTGATCATCAACATCTACAAAAGAGGGAAATTGGCGATTAGCGAGGCC  
CAAGAACATGAGTGGCAGGCTGACTGTCCTGCAAGCAGTGCCTCTCAGAAGAGTC  
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGGAGGCAAAATCATGCCAACAGC  
TTTATCATGTGTTCAAGACCAAGAATCAAGAGCTCTGGATGCCCTAAAAAAATAGCAATG  
**TTAA**CAGTGAACCTGTGTCCTTAAGCTGTATTCTGCCATTGCTTGAAGAGATCTATGTT  
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTGCCAAAGATGG  
GACTGGTGACTCTCACATGATGGAGGTATGAGGCCCTGGAGATAGCTGAGGGAAAGTTCTT  
TGCCTGCTGTGAGGGAGCAGCTATCTGATTTGGAAACCTGCGCAGCTTAGTGCCTGATAGGA  
AGCTAAAGTGTCAAGCGTTGAGCAGCTTGGAAAGCGTTATTATACATCTGTAAAAGGAT  
ATTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTAGAAGTGCAATATTATAGT  
GTATTGTGTTCACTTCAACCCCTTGCCTGAGGTGTACAATCTGTCTGGCTTTCTA  
AACTCAATGCTTAAATAAAATTTAAAGGAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESNDLCRYDFVIVYNGHANGQRIGRFGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVPNGEVNDARRIGKYCGDSSPPAPIVSERNELLI  
QFLSDLSSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## FIGURE 39

CGGACCGGTGGCGGACCGGTGGCGGCCACGGCGCCCGGGCTGGGGCGGTGCGCTTCTT  
CCTTCTCCGTGGCTACGAGGGTCCCCAGCCTGGGTAAGAATGGCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTTCTCAACCTCCAGGACCTATCTGG  
CTCCAGGCCCTCCACCTCCCCAGTCTTCTCCCCGCTCAGGCCCATCCGTGTCATAACCTG  
CCGGGACTGGGTGACAGCTTAACAAGGGCCTGGAGAGAAACCATCCGGACAACCTGGAG  
GTGGAAAACACTGCCTGGGAGGAAGAGAAATTGTCAAATACAAAGACAGTGAGACCCGCTG  
GTAGAGGTGCTGGAGGGTGTGCAAGTCAGACTTCGAGTGCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTACAAGCAGCAGGAGGCCGGACCTTCTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGGGTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAACGGGCTACGGGGTGAGGCCCTGCGG  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACCTGTTGCAATGCAAGAAGG  
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCA  
GTGGAGCTGACCAATTCTCGGTGACACTGAGGGCTCTATGAGTGCCGAGACTGTGCAAG  
GCCCTGCCTAGGTGCTGGGGCAGGGCAGGTGCTGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGTTGAGTGTGAGACAGAGGGTGTCGGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGAGGGCAGATCCAGTCAGCAGGCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGTGCTGAGCAGATGTTGGCATCATCTGTGCACTGGCA  
CGCTGGCTGCTAAGGGCAGTGGTGTGCTGAGGCTTGTGGCCATCTGCTGCTGGGGCATG  
ACTGGCTACTGGTGTGAGGCGCAGTGACGGTGTGCTGGAGGGCTTCAAGGGCAGATA  
ATCGCGGCCACCCACCTGTAGGACCTCCTCCACCCACGCTGCCAGAGCTGGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAAGCACCCCTACCTG  
CCTTACAGAGCAGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAGAAGTAC  
CCTGAAGGTGGATACCATGAGCTCTCACCTGGGGACTGGCAGGCTTACAATGTGTGA  
ATTTCAAAAGTTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGTGGGCCATCACAGCTCCCTCTGCCAGCTGATGCTGCCAGTTCTGT  
TCTGTGTTACCCACATCCCCACCCCATGCCACTTATTATTCATCTCAGGAAATAAAGA  
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPWPKGLVPAVLWGLSLFLNLPPIWLQPSPPPPQSSPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDSERTRLVELEGVCSKSDFECHRLLELSEELVESWWFHQ  
QEAPDLFWQLCSDSLKLCCPAGTFGPSCLPAGTERPCGGYGCQCEGEGTRGGSGHCDCQAG  
YGEACGQCGLGYFEAERNASHLVCACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPEASAGFFSEMTEDELVVLQOMFFG  
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-363

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## FIGURE 41

TGAGACCCCTCTGAGCCTCTCAAGGGACAGCCCCACTCTGCCCTTGCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCTGGGAGCAGCTGCCAGCTGCGCAGCTGAGCTAAAGAGGT  
GCCCACCCCTGGACAGGGCGACATGGAGGAGCTGGTACATCCCCACCCACGTGAGGGCCAGT  
ACGTGGCCCTGCTGCAGCGCAGGCCAGGGACCGCTCCCGGGAAAGAGGTTCAGCCAGAGC  
TTCCGAGAGGTTGGCCGGCAGGGTCTGGCGTTGGAGGCCAGCACACACTGCTGGTGGTCCGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAAGGCCGTCTGGGCTCTTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGGGCTGTCCCCCGCAGGCCCGGGCC  
CGGGTGACCGTCAGTGGCTGCCGTCCCGACGACGGCTCCAACCGCACCTCCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGCTGGAGGCCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCGGAGCCGCTGCTACAGGTGTGGTCAAGAGG  
GAGCATCTGGGCCCGTGGCGTCCGGCCACAAGCTGGTCCGCTTGCTCGCAGGGGGC  
GCCAGCCGGCTTGGGAGGCCAGCTGGAGCTGCACACCCCTGGACCTGGGACTATGGAG  
CTCAGGGCGACTGTGACCCCTGAAGCACCACATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTAATTGACCTGAGGGATGAAGTGGCGAGAACCTGGGTGCTGGAGCCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGCACCTGCCCGCAGCCCCGGAGGCCCTGGCCTCAAGTGGC  
CGTTTCTGGGCCCTGACAGTGCATGCCCTGGAGACTGACTCGCTGCCATGATGTCAGC  
ATCAAGGAGGGAGGCAGGACCAAGGCCAGGTGGTCAGCTGCCAACATGAGGGTGAGAA  
GTGCAAGCTGTGCCCTCGATGGCGCTCGTCCAAGGAGGCTCCAGCCATGGCGCTAGTG  
TAGCCATCGAGGGACTTGAATTGTTCTGAAGTGGTCTGAGGGTACCAAGGAGAGCTG  
GCGATGACTGAACCTGTGATGGACAATGCTCTGTGCTCTAGTGAGGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTGGTCTCTCAGGAATGAGAACATTGGCACTGG  
GAGCCCTGCTCAGTTCTATTCTATTCACTGCACTATATTCAAGCACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGCTCTGTAC  
TGGATCTGGCTAAAGCTCCACCACCACTCTGGACCTAACAGACCTGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTTTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPHVRQAQYV  
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLLPPNSELVQAVLRLFQEP  
VPAKAALHRHGRSPRSARARVTVEWLVRVDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEQPLLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVS LPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## **FIGURE 43**

GTCTGTTCCCAGGAGTCCTTCGGCGGTGTTGTCAGTGGCTGATCCGATGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTCCTTCATATTGGCAGTCCTGTTGCTCCCTGG  
CATTGGGCAGGTACAGTGCACTCTCTGAACCTGAAGTCAGAATTCTGAGAATAACCT  
GTGAAGTTGTCCTGTCCTACTCGGGCTTTCTCTCCCGTGGAGTGGAAGTTGACCA  
AGGAGACACCACCAGACTCGTTGCTATAAAACAAGATCACAGCTCTATGAGGACCGGG  
TGACCTTCTGCCAUACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGAGGTCAAGGTCAAGGCTCATCGT  
GCTTGTGCCUCCATCCAAGCCTACAGTTACATCCCCTCTGCCACATGGGACCGGG  
CAGTGTGACATGCTCAGAACAAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGAT  
GGGATAGTGATGCTACGAATCCCAAAGCCCGTGCCTTCAGCACTCTCTATGCCT  
GAATCCCACAACAGGAGAGCTGGTTTGATGGGACACCCATGACTCAATGCTGTGCGCATGGGAGCT  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAATGCTGTGCGCATGGGAGCT  
GTGGAGCGGAAATGGGGGGTCATGGTGGCAGCCGTCTTGTAACCGTATTCTCTGGGAAAT  
CTTGGTTTTGGCATCTGGGTTGCCTATAGCGAGGGCCACTTTGACAGAAAAGGAAAGG  
CTTCGAGTAAGAAGGTATTTACAGCCAGCTAGGTGCCGAAGGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCCGGTGTGACCCTGGCTCCACCGCCATTCATCTGCATTGCCTTACT  
CAGGTGTACCCGACTCTGGGCCCTGATGTCTGTATTACAGGATGCCTTATTTGTCTTC  
TACACCCACAGGGCCCCCTACTCTTCGGATGTTTTTAATGTCAGCTATGCCCC  
ATCCCTCCTCATGCCCTCCCCCTCCCTCCTACCACTGTGAGGTGGCCCTGGAACTGTTAAA  
GTGTTTATCCCCATTTCTTTGAGGGATCAGGAAGGAAATCTGGGTATGCCATTGACTCCCC  
TTCTCAAGTAGACAGAAAAATGGGGGGGGTCGCAGGAAATCTGCACTCACTGCCCACCTGG  
TGGCAGGGGATCTTGAATAGGTATCTTGAGGTGGCTGGGCTCTTCTGTGACTGTAC  
GACCCAGGGCCAGGTGGCTTAGAGCGGGAATTAGGGGATAGGGGTAGAGCGGGCTGAAAGGTTGG  
TGATGACACTGGGGTCTTCCATCTCTGGGGCCACCTCTCTGTCTCCATGGGAAGT  
CCACTGGGGATCCCTGTCCCTGTCTCCCTGAATACAGGTGACTGAATTTGACTGTGTCTGT  
GGAAAAATGGGGAGGTCTTTGTGGAGAGCAAGTAATTTTCAGAGAACTGAAGCCAAAG  
GATTTAAAAACCCGTCTGAATAAAGAAAGAAACGTGGAGGGCTGGGCGCAGTGGCTCAGGCTCG  
TAATCCCCAGGGGTGGAGGCAGGGGTCACTGTAGGGATGGGTGGATCAGGTCCGTACCA  
ACATGGGAAACCCTACTGGAAATACAAAGTTAGCCAGGTGGGTGGGTCAGTGCCTGTAGTC  
CCAGGTGCTCAGGGAGCCCTGGCAACAAAGGACAAAACCCAGGTCAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSAYSGFSSPRVEW  
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCTMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIVSQPSARSEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## **FIGURE 45**

CAGCGCGTGGCCGGCGCCGTGGGGACAGC**TGAGCGGC**GGTTGGATGGCGCAGGTTGGA  
CGTGGCGAACAGGGCTCTGGGCTGGCGCTGCTGCTGCTCGCCTCGGACTAGGCCT  
GGAGGCCGCGAGCCGCTTCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG  
GCTCGTGCACCCACCAAGTCCAGTGCACCGACCAGTGGCTTATGCGTGCCTCACCTGG  
CGCTGCGACAGGGACTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACGCCCTGGCTCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCACTGCAGGCCCTGGCCTGCCCTAGCA  
GGCGAGCTCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGTGCAGGCCA  
CCCAACTGTCCCGACTCCAGCGACGAGCTGGCTGTGGAAACCAATGAGATCCTCCCGAAG  
GGGATGCCACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC  
ACACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTGGAAATGCCACATCCTC  
CTCTGCGGAGACCGACTGGAAGCCAACCTGCCTATGGGTTATTGCAGCTGCTGCGGTGC  
TCAGTGCAAGCTGGTACCCGCCACCCCTCCCTTGTGCTGGCTCCGAGGCCAGGAGC  
CTCCGCCACTGGGTTACTGGTGGCATGAAGGAGTCCCTGCTGTCAGAACAGAAC  
CTCGCTGCC**TGAGGACAAGC**ACTTGCCACCCGTCACTCAGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGTACCCGGCACCCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAAC  
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLGLGLCLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCDRDLCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL  
RNCSRLAACLAGELRCTLSDDCIPLTWRCGDHPDCPDSSDELGCGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPVGNAATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## FIGURE 47

CCACCGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGAGCAGAGGTCCGCACAGATGCGG  
GTTAGACTGGGGGGGGAGGAGGCGGAGGAGGGAGGAAGGAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAGCTGGATGCCCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTCAAGCTGGCGCTGTGCTTCGCCCTGCACAGCTCACGGGGGTT  
CGATGACCTCAAGTGTGTGTCGACCCGGCATCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTCTTGAAGGCTCTGTAGCCCATTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAACTGA  
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAATCGAAGATGCTGAGATTCTATA  
ACAAGACATATAGACATGGAGAGAAGCTAACTCATCACTTGTCAAGGATTCAAGATCCGG  
TACCCCGACCTACACAATATGGTTTCAATTGTGGATGATGGAACGTGGATAATCTGCC  
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCTCTTCAATGGCTATGTAACATCTCTGAGC  
TCCAGACCTCCTCCGGTGGGACTGTGATCTCTATCGCTGCTTCCGGATTAAACTT  
GATGGGTCTGGTATCTTGAGTGCTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG  
CCTTGCCTGGAAGCCCAAGCTGTCCACTACCTCAATGGTAGTCAAGGAGATTCTCT  
GCCACCCGCGGGCTTGTGAGCGCTACAACCAAGGAACTGTGGTGGAGTTTACTGCGATCCT  
GGCTACAGCCTACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC  
TTATCAAGTCACTGCATCAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTGCTCGTCATC  
CTGGCCAGGATTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG  
TTCCAGCAGTGACCTGACTTGTGGTGGTAGACGGCGTGCCTCATGCTCCGTCATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGTACATGGCTCTGTGGCCAG  
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGGACCGGA  
CACAGGCCAGGGAGTCAGAAAACCTGTGACAGCGTCAGGCTCTCTGAGCTGCTCCAAA  
GTCTGTATTCACTCCCAAGGTGCAAGAGAGCACCCACCTGCTCGGACAACCCCTGACATA  
ATTGCCAGCAGGCCAGAGAGGTGGCATCCACCAAGGCCAGGATCCATCATGCCCACTGGT  
GTTGTTCTAAGAAACTTGATTGATAAAAAATTCCAAAGTGTCTGAAGTGTCTCTCAA  
ATACATGTTGATCTGTGGAGTTGATTCCCTTCTCTGGTTTAGACAAATGTAACAA  
AGCTGTGATCTTAAATTGCTATGCTGATAGAGTGGTGAAGGCTGGAGCTTGATCAAGTC  
CTGTTCTTCTTGACACAGACTGATTTAAAGNAAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLQQQQQQPQSPQRLLAVILWFQQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKAGTKRLCLKHFNGLGWI PSDNSICVQEDCRI  
PQIEDAEIHNKTYRGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPI CQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKITYTCQYGEWFPSYQVYCIKSEQT  
WPSTHETLTTWKIVAFATSVLLVLLVILARMFQTKFAHFPFRGPPRSSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## **FIGURE 49**

CCCCACGCGTCCGCTCCGCCCTCCCCCGCCCTCCCGTGCCTGGCTGGCTAGAGA  
TGCTGCTGCCGGGTTGCAGTTGCTGCCACGCCCTCTGCCCGCCAGGCCCTCCACGCCGT  
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCGCGCTACAGG  
CCGTGCTGCTGGCGTGTGCTGGTGGGCTGCGGGCCGCGACGGGTCGCTGCTGAGTGCC  
TCGGATTGGACCTCAGAGGAGGGCAGGCCAGTCTGCCGGGAGGGACACAGAGGCCCTGTTA  
TAAAGTCATTTACTTCATGATACCTCTCGAAGACTGAACTTGAGGAAGCCAAAAGAGCCT  
GCAGGAGGGATGGAGGCCAGTCAGTCAGCATCGAGTCGAAGATGAAACAGAAAAGTGTAGAA  
AAGTTCATGAAAACCTCTGCCATCTGATGGTACTCTGGATTGGCTCAGGAGGCCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGACTGATGGCAGCATAT  
CACAAATTAGGAACTGGTATGGATGAGCGTCCCGCCAGCAGGAGGTCTGCGTGGTCATG  
TACCATCAGCCATCGGCCAGCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA  
CCGGTGCAACATGAAGAACATTCTTTGCAATATTCTGATGAGAAACAGCAGTTCCCT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG  
GAAGAAGATGCCAAAAACATTAAAGAAAGTAGAGAAGCTGCCTGAAATCTGCCCTACAT  
CCTAATCCCCAGCATTCCCTCTCCCTCCCTGTGGTACCCAGTTGTATGGTTGGTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAAGCAACACCCATC  
TGGCCCTCTCCCTCACCGGGAAACAGCCCGACCTAGAGGTCTCACATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAATATTCTTCAGGTGTGTT  
CGGGAGAAGCCACTCCCGATGACATGCTTGTGACTATGACAACATGGCTGAAACCCATCA  
GAAAAGTGGTTGTGACTCTGGTGAGCGTGGAGGTGGATTGTGACCAATGACATTATG  
GTTCTCCCCAGACCAAATGGGAGGAGTAAGGAGTCTGGATGGGTGAAAATGAAATATG  
GTTATTTAGGACATATAAAAACTGAAACTGACAACATGGAAAAGAAATGATAAGC  
AAATCTCTTATTTCTATAAGGAAAATACACAGAAGGTCTAGAACAGCTTAGATCAGGCTCTG  
GGATGAGCATGTTGGCCCCACGACCTCTGGTGGACCCCCACGTTGGCTGTATCTTTAT  
CCCAGCCAGTCATCAGCTGACCTTATGAGAAGGTACCTTGCCCAAGGTCTGGCACATAGTA  
GAGTCTCAATAATGTCACCTGGTGGTGTATCTAACCTTAAAGGACAGAGCTTACCTG  
GCAGTGTAAAGATGGGCTGTGGAGCTGGAAAACACCTCTGTTCTGCTCTACAG  
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGGCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCATTCTCATATCTGTTTTCAAGAATAAAATCAAATG  
GCAGGAAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDDLRLGGQPVCRGGTQRPCYKVIYFHDTSRRL  
NFEAKEACRRDGGQLVSIESEDEQKLIKEKFIENLLPSDGFwigLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY  
SDEKPAVPSREAEGEETELETPVLPTEETQEDAKKTFKESREAALNLAYILIPSIPLLLLLV  
VTIVVVCWVWICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLVSVESGFVTDIYEFSPDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGTCCCTGCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCTCTGCAGCCTAACCGGAGGGCAGCGAGGGCTTACCAATGATCATGGTGT  
GTCAGCATGCGCTGTGGACCCCAGTGGCGCTCGACCTCGTGGCTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTCTGTTGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTTCCACCCCAAACTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTTGTGGCAGCTGACCAAGGTGGCAT  
GCAGCAAATGTTGCCTGGAGAGAGACTGAGGAAGAACTATGTGGAGACATTCCCTTC  
TTTCACCAACCTTCAACCCACAGGAGGTCTTATTGCTTCCACTAACATTTCGGAATCTG  
GAGTCCACCCGTTGTTGCTGGCTGGCTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTCAAGTCTGTATCCAAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACAGAGGGCGGAGGCAGACTGCCCTTTACAGGCCAGGAATCTCAGAGGATTG  
AAAAAGCTGAAGGACAGGATGGCATTGACAGTAGTGTAAAGTGGACTTCTTCATCTCCT  
GGACAACGTTGGCTGCCAGGACACACACCCAGCTGCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG  
TGACCTTCATACCGCTTAAATGACCCCTGGGATTGGTACCAAAATGGCCACCGTTGCT  
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAAGCTCTA  
TTACACGGGAAGGAGCAGGTGCCAGAGGGTGTCCCTGATGGGCTCTGCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTTACCTTAAGCCCAGAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAGTGCCTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRH GAR  
SPLKPLP LEEQVEWNPNPQLLEVPPQQTQFDYT VTNLAGGPKPYS PYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRK NYVEDIPFLSPTFPNPQEV FIRSTNIFRNLESTRCLL AGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRRQTA SLPQPGISEDLKKVKDRMGIDSSDKVD  
FFI LLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYI LPKEDRESLQMAVGPF LHI LES  
NLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTL GIFDHKWPFFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSPEKYHALCSQTQVMEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTTGGGACCTCCTCTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTGACCAGACCTGGATTCTAGCGCTCCATCTGGAGTGCAGCTGGTGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGACCGTGTGATG  
ACGGCTGGACATTAAGGACGGCTGTGTTGTGCCGGAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTGTATGAGGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCCTTTCTCCCCA  
GTCCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGGTGGAAAGTGA  
GCACCAAGAACAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCGGGCCAAAGGTGG  
TGTGCCGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAACCCATCTGGCTGAGCCAGATGTATGCTCAGGACGAGAAGCAACCTTCA  
GGATTGCCCTCTGGGCCTGGGGAAAGAACACCTGCAACCATGATGAAGACACGTGGTCG  
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGCTCTGCTGTGATGACAATGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGCTGTGGGAAGTCCTCTCCTCAGAGACCGGA  
AATGCTATGCCCTGGGTTGGCGCATCTGGCTGGATAATGTTGCTCAGGGAGGAG  
CAGTCCCTGGAGCAGTGCACAGATTTGGGGTTTCACGACTGCACCCAGGAAGA  
TGTGGCTGTATGCTCAGTTAGGTGGCATCATCTAATCTGTTGAGTGCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAAACTGATCT  
TCTTCTGCCCTGGACTGGACTTAACTTGGTGCCTCTGATTCTCAGGCCTCAGAGTTGG  
ATCAGAACCTAACACATCAGGCTCTAGTTCTCAGGCCATCAGACATAGTTGAAACTACATCA  
CCACCTTCATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTTAT  
CAACTACTTAAACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCATTTGTCCTGTTCTCTGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTAAAGATAATTCTGAATTGGTTATGGGTTCTGAATTG  
GCTCTATAATCTAATTAGATAAAAATTCTGGTAACCTTATTACAATAATAAAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFLSLILAICTRPGLASPVGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVL  
RELGCAGAASGTPSGILYEPPAEEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNWYTCQTGWSLRAAKVVCRQLGCCRAVL  
TQKRCNKHAYGRKPILSQMSCGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSRLEVHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## FIGURE 55

ACTGCACTGGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACCGCGTCCCGGGACCGTGGCGGACCGTGGCCGCTACCCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCCATCACCTCCACAGGCATCCTGCCCTGCTGTTGGCTGCCCTGGG  
CGTCTTCGGCCTCTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCACCTGCCGAATGCTG  
TGGTGGTGTACAGCGCCACCTCAGGGCTGGCAAAGAAATGTGCAAAGTCTTCTATGCT  
GCGGGTGTAAACTGGTGCTGTGGCCGAATGGTGGGGCCCTAGAAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCCTGGCTATGTC  
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGTACCATCATGGACACACAGTGG  
TGTGGACAAGAGGGTCACTGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC  
TGCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGAA  
CTGCTCGGTGCCAGATGAAACAGTATGAAATTGAGGTGACCGTCATCAGCCCGGCTACA  
TCCACACCAACCTCTCTGTAATGCCATACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCAACACAGGCCAGGGCGAAGGCCCTGTGGAGGTGGCCAGGATCTTGTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCTGGCTGACTTACTGCCTCCTTGGCTGTTTATCTCGAA  
CTCTGGCTCTGGCTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAAGCAGCAGTCTTAGGTTGC  
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGTCTCACAAAGTGGG  
AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCGAGGGACAATAAAAACGACAACA  
AGCTTCTCCCAGGGTGGGGAAACACTTAAGGAATAAAATATGGAGCTGGGGTTAACACT  
AAAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAGGGCGGCCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCAACCTGTTATTGCAGCTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPVLVTFDLTDGAI  
VAAAEEILQCFGYVDIL  
VNNAGISYRGTIMDTTVDVDKRMETNYFGPVALT  
KALLPSMIKRQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLA  
AVGKKKD  
VILADLLPSL  
AVYLRT  
LAPGLFFS  
LMA  
SRARKER  
KSNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## **FIGURE 57**

CCACCGCGCCGCTGGTGTAGATCGAGCAACCCCTAAAGCAGTTAGAGTGGTAAAAAA  
AAAAAAAAACACACAAACGCTCGCAGCCACAAAGGGATGAAATTCTCTGGACATCCTC  
CTGCTTCTCCGTTACTGATCGTCTGCCAGAGTCCTCGTGAAGCTTTTATTCTAA  
GAGGAGAAAATCAGTCACCGCGAAATCGTCTGATTACAGGAGCTGGCATGGAATTGGA  
GACTGACTGCCTATGAATTGCTAAACTTAAAGCAAGCTGGTCTCTGGATATAAAG  
CATGGACTGGAGGGAACAGCTGCCAATGCAAGGGACTGGGTGCAAGGTTCATACCTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTAATGCACTTCCTGGACTACAAA  
GGCATTTCCTCCTGCAATGACGAAGAATAACCATGGCCATTGTCACTGTGGCTCGGCAG  
CTGGACATGTCGGTCCCCCTCTTACTGGCTTACTGTTCAAGCAAGTTGCTGCTGTTGGA  
TTTCATAAAAACCTTGACAGATGAACTGGCTCCTACAAATAACTGGAGTCAAACACATG  
TCTGTGTCCTAATTGTAACACTGGCTCATCAAAATCCAAGTACAAGTTGGGACCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGATGGATTCTGACTGAGCAGAAAGATG  
ATTTTTATTCCATCTCTATAGTTTTAACACATTGAAAGGATCCTCTGAGCGTT  
CCTGGCGTTTAAACGAAAATCAGTGTAAAGTTGATGCACTTATTGGATATAAAATGA  
AAGCGCAAAGCCTAGTTCTGAAAAGTGAATTACCAAGGTTAGGTTGATGTCATCTA  
ATAGTGCAGAATTAAATGTTGAACCTTGTTCTAATTATCCCATTCTCAATA  
TCATTGGAGGCTTGGCAGTCCTCATTACTACCACTGTTAGCCAAAGCTGATT  
ACATATGATATAAACAGAGAAAACCTTAAAGGTGACTTAAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTTATTAAATAATTCCAAGATTGTTGAGGCTCACCTGAAGGCTTGC  
AATTGTAACATAACCGTTTATTAAACATATTTTATTGATTGACTTAAATTGTTG  
ATAATTGTTGTTCTTTCTGTTCTACATAAAATCAGAAACTTCAGCTCTAAATAAAA  
TGAAGGACTATATCTAGTGTATTTCACAAATGAATATCATGAACTCTCAATGGTAGGTT  
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACTCACATTCAATGCCAAACATTCT  
GCACAGGGAGCTAGAGGTGGATACAGTGTGCAAGTAAAGCATCACTGGATTAAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAA  
AA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 58**

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDLFLATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## FIGURE 59

CCACCGCTCCGGAGCGCTGGTCGACTAGTTCTAGATCGCGAGCGCCGCCGGCTC  
AGGGAGGAGCACCGACTGCGCCGACCCCTGAGAGATGGTTGGTGCCTGTGGAGGTGATTG  
TTTCGCTGGCTCTGGTATGCCCTGGCCCTGTGATGGGCTTTCGCTCCCTATACAGAAAGT  
GTTTCATGACCTAAGGGAGACTCAGGACAGCATTATTCCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGCTGGCCCTTCCAGGACTGAACATGA  
AGAGTTATGCCGGCTTCTCACCGTGAATAAGACTTACACAGCAACCTCTCTGGTT  
TTCCAGCTCAGATACAGCCAGAAGATGCCAGTAGTTCTCTGGTACAGGGTGGCCGG  
AGGTTCATCCATGGACTCTTGTGGAACATGGGCTTATGTTGTCACAAGTAACATGA  
CCTTGCCTGACAGAGACTCCCGGACCAACAGCTCCATGCTTACATTGACATATCCA  
GTGGGCACAGGCTTCAAGTTACTGTATGATAACCCACGGTATGCACTGAGGACGATGT  
ACCAAGGGATTATAACAGTCACTAATTCAAGTTTCCAGATATTCTGAATATAAAATA  
ATGACTTTATGTCACTGGAGCTTATGCCAGGAAATATGAGGGCAGCCATTGCAACACCTC  
ATCCATTCTCAACCTGTGAGAGGGTGAAGATCAACCTGAACGGAAATTGCTATTGGAGA  
TGGATATTCTGATCCCGAATCAATTATAGGGGCTATGAGAATTCTGTACCAAATTGGCT  
TGGTGGATGAGAAGAAAAAAAGTACTTCCAGAAGCAGTCCATGAATGCAAGAACACATC  
AGGAAGCAGAACACTGGTGGAGCTTGAATACTGGATAAACTACTAGATGGGAGCTTAAC  
AAGTGTACTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGGGT  
GCACGGAACCTGGAGGATCAGCTTACTATGTGAAATTGGTCACTCCAGAGGTGAGACAA  
GCCATCCACGGGGATCAACGACTTAACTGGATAAGTGGAAATATGTTGAGAAGTACTTGGAGA  
AGATAACAGTACAGTCAGTTAACGGCATGGTAACTGAAATCATGAAATAATTATAAGGTCTGA  
TCTACAATGGCAACTGGACATCATGTCAGCTGCCAGACAGGGCTCTTGATGGC  
ATGGACTGGAAAGGATCCCGGAATACAAGAAGCAGAAAAAAAGTTGGAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTACATCCGGCAAGCGGGTGAATTCCATCAGGTAATTATTC  
GAGGTGGAGGACATATTACCCATTGACCCAGCTCTGAGAGCTTGTGACATGATTAATCGA  
TTCATTATGGAAAAGGATGGATCCTTATGTTGATAAAACTACCTCCAAAAGAGAACAT  
CAGAGGTTTCATTGTCAGAAAAGAAAATCGTAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATTCGCAAGATTTTTCAATCAATAAAATTATCCTGAAACAAGTGAGC  
TTTGTGTTTGGGGGAGATGTTACTACAAAATTACATGAGTACATGAGTAAGAATTACA  
TTATTAACCTAAAGGATGAAAGGTATGGATGATGTGACACTGGAGACAAGATGTATAATGA  
AATTGAGGTCTTGAATAGGAAGTTTAAATTCTCTAAGAGTAAGTGGAAAAGTGCAGTTG  
TAACAAACAAAGCTGTAAACATCTTCTGCCAATACAGAAAGTTGGCATGCCGTGAAGGT  
GTTTGGAAATATTGGATAAGAATAGCTCAATTATCCAAATAAATGGATGAGCTATAA  
TAGTTTGGGGAAAAGATTCTCAAATGTATAAGTCTTGAACAAAAGAATTCTTGAAATA  
AAAATATTATATAAAAGTAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGREL  
SVPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLDRDRDPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEEDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPKREVKINLNNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFPEAFEILDKLLDGDLTSDPYFQNV  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNGQTFNDGTIVEKYLREDTVQSVKPWL  
EIMNNYKVLIYNGQLDIIVAALTERSLMGMDWKGSQBYKKAEKKVWKIFKSDSEVAGYI  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTCCGGCTCCGGAATGGCACATGTTGGGAATCCAGTCTGTTGGCTACAAACAT  
TTTCCCTTCTTAACTAACAGCTGTTAACAGCTAGTCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGTGACCAGCTCTT  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGAGGGAGTGAGGTGATGGAAG  
TCTAAAGTAGGAAGGAATTGTCAGACTCTGGGAGGAGCTTGACCTGGAGAGC  
CTGGGGAGGGCTGCTAACAGCTTCAAAAAACAGGAGCGACTTCACTGGCTGGGAT  
AAGACGTGCGGTTAGGGAGACTGGGTTAGTCTAATATCAAATTGACTGGCTGGG  
TGAACCTTCAACAGCCTTTAACCTCTCTGGAGATGAAACGATGGCTAAGGGCCAGAAA  
TAGAGATGCTTGTAAATAAAATTAAAAAGCAAGTATTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATCTCTGAACTTCTAACAGGGAGAAAGTATGTTAAATAA  
GAAAAACCAAAATGCAAGAGGAGACTCACAGAGCTAACAGGAGTGGGACCTGGGTC  
AGGCCAGCCTCTTGTCTCCCGAAATTATTTGGTCTGACCAACTCTGCTTGTGTTT  
GCAAAATCATGTTGAGGGCAACCGGGGAAGGGAGCATGAGCACACAGGAGCGCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG  
ACAGCGCCTGTGCTCTGCTCATGTTGCTGGTCTGGTCTGGCCCCCAGCAGCCG  
ATGCTCTGAGTCAGCACCCTTCACTCTGAGAACATCTGACCTGGACCTAACCAACTTGACCGT  
CCACCAAGGGACGGGGCCGCTATGTGGGGCCATCAACGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCAGGTGGCTATAAGACAGGGCAGAAGAGGACAACAAGTCTCGTACCCG  
CCCTCATCGTCAGCAGGCTCAGCGAAGTGTCTACCCCTACCAAAATGTCACAAAGCTG  
CATCATTGACTACTCTGAGAACGGCCCTGCTGGCTGTGGAGGCTCTAACAGGGGCTG  
AGCTGCTGCGGCTGGATGACCTTCTCATCTGGTGGAGGCATCCCACAAAGAAGGCAACTAC  
CTGTCAGTCTCAAAAGACGGGACCATGTCAGGGTGATTGTGCGCTCTGAGGGTGGAGA  
TGGCAAGGCTCTCATCGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCCTG  
GCCGGAAAGCTGCCCGAGACCCCTGAGTCTCAGCCATGCTGACTATGAGCTACACAGCG  
TTTGTCTCTCTCATCAAGATCCCCCTCAGAACCCCTGGCTCTCCACTTTGACAT  
CTTCTCATCTACGGCTTGTAGTGGGGCTTGTCTACTTCTCATGTCAGCCGAGA  
CCCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCCCTTCTACACCTCAGC  
CATCGTGC  
CTCTGCAAGGATGACCCCAAGTCCACTCATCGTGTCCCTGCCCTCGCTGACCCGGG  
CGGGGTGGAAATACCGCCCTCTGAGGCTGCTTACCTGGCAAGGCCCTGGGACTACTGGCC  
AGGGCTTCAATATCACAGCAGGAGCATGTACTCTTGCATCTTCCAAAGGGCAAG  
CAGTATCACCAACCCGGCGATGACTCTGCTGTGCTTCCCTACCGGGCATCAACTT  
GCAGATCAAGGAGCGCTGAGTCTGTAACAGGGCGAGGGCAACCTGGAGCTAACCTGG  
TGCTGGGGAGGAGCGTCCAGTCCAGGAGGCGTCTGGGAGGCTACAGCTGTTT  
CTGGACATCAACCAAGCCCTGGAGGCTCAACTCCAGTGGAGGCTGACCCCTGACACAC  
CAGCAGGGACCGCATGACCTCTGTCCTCTACGGTTAACCGGCTACAGCGTGGTTT  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAAGTGCCTCAATGCC  
ATTCACCTCTCAGAAAGAGTCCCTCTGGAGGAGTAGCTATTGGTGGAGATTAACCTAG  
GCAACTTATTTCTGGGAACAAAGGTGAATGGGGAGGTAGAAGAAGGGTTAATTTG  
ACTTAGCTCTAGCTACTTCCAGGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA  
TTTCAATATTCACCAACTTAAAGAAAAACTTAAAGAAGGTACATCTGCAAAGCAA

## **FIGURE 62**

MGTLGQASLFAPPGNWFWSDHSAACFAESCEGQPGKVEQMSTHRSRLTAAPLSMEQRQPWP  
RALEVDSDRSVVLLSVVVWLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNGNLTQVAHKTGPEEDNKSRYPPLIVQPCSEVLTNTNNVNKLIIIDYSENRLACGSL  
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNVKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLPDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSHYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFAIFSKGQKQYHPPDDDSALCAFPIRAINLQIKERLQSCYQGEGN  
LELNWLLGKDQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTGKSLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCCGCGCGCGCTGAGTGCGGACTGGAGCTGGGAAACCGGGTCCCGCGCCTTAGAGAACACCGCATGACCA  
CGTGGAGGCTCCGGCGAGGCCGGCCGACGCTGGGACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCC  
GCAGGGCTGAGACTGGAGCACCCCTGGTCCCTCTGGGCTCGGCCATCGACAGCTGGGCTGAGGCCAACGGCTGGA  
ACTCTATGCTGGAGGACCTGGACCTTCTGGGACTCTGGGCTGAGCTGGGACTTCTGGGCTGACACCCCTAACACCTATG  
GGAGGGACGCCCTGTAAGATGAAGGCTGTGGCTGACACCCCTAACACCTATGTCGTGAAACCTGATCG  
AGCCAGAAAGAGGCAAAATTGACTCTCTGGGAACTGGACCTGGAGCCCTTCTGTCTGATGGCCGAGAGATCG  
GGCTGTGGGTGATTCTGCCTCAGGCCCTACATCTGCACTGAGATGACCTCGGGGCTGCCCCAGCTGGCTAC  
TCCAAAGACCCCTGGCATGAGGCTGAGGAAACCTTACAAAGGCTTACCGGAAGCAGTGGACCTTTATTTGACCAAC  
TGATGTCCAGGGTGGTGCACCTCCAGTACAAGGCTGGGGACCTTATCTGGCGTGCAGGTGGAGAAATGAAATG  
GTTCTATAATAAAGACCCCGCATACATGCCCTACGTCAGAAGGCACTGGAGGACCGTGGCAITGTGAAACTG  
TCCTGACTCTAGAGAACACAGGATGGCTGAGGAGGATTTCTGGAGGAGCTTCTGGCACCCATCAACTTCCAGT  
CAACACAGGACTGGCTGAGCTGACCCACTTCTCTTCACGTCAGGGACTCAGGCCAACATGTTGATGGAGT  
ACTGGACGGGTGGTTGACTGCTGGGAGGCCCTACAAATATCTGGATTTCTGGAGGTTTTGAAAAACCGTGT  
CTGGCAITGTGGACGCCGGCTCTCCATACACTCTACATGTTCCACGGGACCCAACTTGGCTTCAATGAAATG  
GAGCCATGACTTCCATGACTAACAGTCAAGATGTCACGACTGATGACTATGATGCTGTGACAGAACGGCG  
ACCTTCTCCAAAGATGCGGCTATGAGGCTTAAACGGCTGACTCTGGACTCTCAGGCACTCCCTCCCCAACCTG  
ACCTTCTCCAAAGATGCGGCTATGAGGCTTAAACGGCTGACTCTGGACTCTCAGGCACTCCCTCCCCAACCTG  
TGGGGAGACCAATCAAGTCTGAAACCCCAATCAATGGAGAACCTGGCAGTCAATGGGGAAAATGGACAGTCT  
TCGGGACATTCTCATGAGCACGACCATCCTCTGTCGGCAGCTGTCAGTGGCACCTGCAATGATGGGGGAG  
TGGGGAGACCAATCAACCCAGGCTTACTGGAACTTGGGACCCAGAACGACGCTTACCTCCAGGCTCTGGTGA  
GCAGGGAACTAACCAACGGTCACTGGTTTGAGGAGCACATGGGGGGCTCTGCAATTACAGTCAAGGAAACCCCC  
ACCTGGGCAAGGAAACGGTACATTAAGT~~GA~~GCGTGGCACCCCCCTCTGGTGGCAGTGGAGACTGCCCTC  
CTCTTGAGCTGAGACCTGGTGGCTGCTGCCACCCCTACTGCAAAAGCATCTCTTAAGTAGCACAACCTCAGGG  
ACTGGGGGCTACAGTCTGGCTCTGTCAGCTAAACCTTAAGCTGAGGGAAAGGTGGGGATGGCTCTGGGG  
TGGCTTGTGATGATGCTTCTCACGCCCTGCTCTGTCGGCAGGGCTGTCGGGCTGTCAGGGGGAGC  
AGCTAATCAGATGCCAGGCCAGCTTGGCCTTCAAGAAAAGTGTGAAACGTGCCCCCTGCAACGGAGCTCACGCC  
TCGGAGCATCTGGTCACTGGCTGCTCTGGCTGTTCTGGAGGCTTGGCACACTCCCTCATGGCCCAT  
TTATCCCCAAATCTGGGTGTCACCTGGTGAAGGGTGGGAAGGGGTGTCACCTGAGCTGACTTGGTT  
CTTCTCCACACCTGAGACCTCTGGGATTCTGGAAAGACTGGCTGAGAACATCTCACCTGCGTCTCC  
TCCCTTCCCACCTGCTGCCACAGGGTACAGGGCTGGGCTGAGAACACAGAAATCTCACCTGCGTCTCC  
CAAGTTAGCAGGTCTGGTGTGTCAGTGGAGGAGACATGTGAGCTCTGGCAGAACAGCCTGGCCCATGTCGCA  
CATCCAGGGAGGAGCACAGGCCAGCTCACATGTGAGCTGGCAGAACAGCCTGGCCCATGTCGACATCAGGG  
AGGGAGGGAGCACAGGCCAGCTCACATGTGAGCTGGCAGAACAGCAGGGAGGAGCACAGGCCCATGTCGACATCAGGG  
GGAGGAGCACAGGGGAGCACAGGCCAGCTCACATGTGAGCTGGCAGAACAGCAGGGAGGAGCACAGGCCCATGTCGACATCAGGG  
ACAGAAGGCCAGCTGAGGCCCCGCTCCACCCCCACGCCGAACAGCAGGGAGGAGCACAGGCCCATGTCGACATCAGGG  
GAAGTGTGTCAGTCCAACTGGCAATTGAGCCTTGTGGGGGCCCCAGGCCAACACCTGGCTGGCTACTGCTCTGA  
GTTGCAAGTATAACCTGATCACAA

## **FIGURE 64**

MTTWSLRRR PARTLGLLLL VVVLGFLVLRRL DWSTLVPLRLRHRQLGLQAKGWNFMILEDSTFW  
I FGGSIHYFRVPREYWRDRLLKMKACGLNTLTTVVPWNLH EPERGKFD FSGNLDLEAFVLM A  
AEIGLWVILRPGPYICSEMDLGGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLM SRRVPLQ  
YKRGGPIIAVQVENEYGSYNKDPA YMPYVKKALEDRGIVELLTS DNKG DLSKGIVQGVLAT  
INLQSTHELQLLTTFLNVQGTQPKMVMEYWTGWFDSWGGPHNILDSS EVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP  
LPPPPDLPKMPYEPLTPVLYLSLWDALKLGEPIKSEKPINMENLPVNGGNGQSFYI LY  
TSITSSGILSGHVHD RGQVFVNTVSIGFLDYKTTKIAVPLI QGYTVLRLVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFGLDKWXSLP EPTPLPAFFLGSLSIS  
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSG I NQVIVFEETMAGPA  
LQFTETPHILGRNQYIK

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGAGGGGTGGACGGGTCAGGACCCAGGACCTCGGGCTTCAGGACGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGGCTCGGGCCAGGGCCCCCAGGACCTTCATCTCCAAATGTTGGAGGAATC  
CGACACGTGACCGTCTGGCCCGTCTCAGACTAGAGGAGCGCTGTAAACGCC**ATGGCT**CCC  
AAGAACGCTCTGGCTCTGGCTCTGGCTAGTGATAGGGGTCTAGCCCTGACCTACTGCTGCC  
GGCAGACACTCGGTGCTGGCTAGTGATAGGGGTCTAGCCCTGACCTACTGCTGCC  
CGTTCGCTATGTGCTGGCAGCCTGCACTACTTCTGGGTACCGCGGGTCTGGCCGAC  
CGGCTTTGAAGATGCGATGGAGCGCTCAACGCCCATACAGTTTATGTGCCCTGGAAC  
CCACGAGCCACAGCCTGGGTCTATAACTTTAATGGCAGCGGGACCTCATTGCC  
ATGAGGCACTGAGCTCTAGCGAACCTGTTGGTCACTACTGAGACCCAGGACCTTACATCTG  
GGAGATGGGGGCTCCCATCTGGTGTCTGGAAACCTGAAATTCTAAGAACCTC  
AGATGCCAGACTCCCTGGCCAGTGAGCTCTGGTCAAGGTCTGGCTGCC  
CATGGCTTATCACATGGGGCAACATCATTAGCATTAGGTGGAGATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTCTCCGTGCACTGCTAGG  
AGAAAAGATCTGGCTTCCACACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCCGG  
GACTCTATACACTGTGATGATTGGCCAGGCTGACAACTGACCAAATCTTACCCCTGCTT  
CGGAAGTATGAACCCCCATGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGTGGATT  
CTGGGGCAGAACATCCTCACCCACAGGCTGTGCTAGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTGGGGCAGGTGAAACATGTAATGTTCCATGGAGGTTACCAAATTGGATATTGG  
AATGTTGCGATAAGAAGGGCAGCTTCTGGATTACTACAGCTATGACTATGATGC  
TATATCTGAAGCAGGGGACCCACACCTAACGTTTGTCTTCGAGATGTCTCAGCAAGT  
TCCAGGAAGTCTTGGGACCTTACCTCCCGAGGCCAAGAGTATGCTTGACCTGTG  
ACTCTGCACTGGTTGGCATTACTGGCTTCTCTAGACTCTGCTTGGCCCGTGGGGCCAT  
TCATTCAATCTGCCAATGACCTTGGAGGCTGTCAGCAGGACCATGCTCATCTGTAC  
GAACTTATGACCCATACCATTTGGAGGCAACACCATTCTGGGTGCAAATATGGAGTC  
CATGGCTGCTATGTGATGGTGGATGGTGGCTCAGGGTGTGGAGCGAACATGAG  
AGACAAACTATTGGAGGGGAAACTGGGCTCAAACCTGGATATCTGGTGGAGAACATGG  
GGAGGCTCAGCTTGGCTAACAGCAGTGACTTCAAGGGCTGTTGAAGCCACCAATTCTG  
GGCACAACATCTTACCTGGAGGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
GTGTTTCCCTCCAGTGGCAAAATGGCCTATCTCAAGCTCCTCTGGCCCCACATTCT  
ACTCCAAACATTTCAATTAGGCTCAGTGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACCTGGGGTACTGGACAAAGCAGGGCC  
AAACAGACCTCTACGTGCAAGATTCTGCTGTTCTAGGGGACCCCTAACAAAATTA  
CATTGTGAACTAGAAGATGACCTCTCAGGCCAACATCAATTCCCTTCACTGGCT  
CTCAATAGCAGTACTGTTGACAGGACACATTAATCTGGGAGGCTTACCTGGAGTC  
TGCCTCTGAACCAATGGAGTTAAGTGGGCACT**GAAGGTAGGCCGGCATGGTGGCT**CATGC  
CTGTAATCCAGCAGTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTC  
CCAGCCTGGCCACATGGTAAACCCCGTCCACTAAAAAATACAAAATTAGCCGGCGTG  
ATGGTGGGACACTCTAATCCAGCTACTGGGAGGCTGAGGGCAGGAGAATTGCTTGAAATCC  
AGGAGGCAAGAGTTGCACTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGTGACAGTGA  
GACACTCCATCTCAAAAAAA

## **FIGURE 6**

MAPKKLSCRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKGCSRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLWQGNHSTRSVSAVTKGLENMLKLGASVNMYMFHGGTNF  
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPPTFWVPN  
NGVHDRVAYVMVDGVFQGVVERNMGRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTIILTQWMMFPLKIDNLVKKWFPQLPKWPYPQAPSGPTFYSKTFFPILGSVGDFFLYL  
PGWTKGQVWINGFNLGRYWTKQGPQQTLVYPRFLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCCTTGAAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGCA  
ACCCACAATATGGCTTACATGTTGAAAAAGCTCTCATAGTTACATATCCATTATTTGTGT  
TTATGGTTTATCTGCCTCTACACTCTTCTGGTTATTCAAGGATACCTTGAAGGAATATT  
CTTCGAAAAGTCAGAGAAGAGAGCAGTTTAGTGACATTCCAGATGTCAAAACGATTT  
GCGTTCCCTCTCACATGGTAGACCAGTATGACCAGCTATTCCAAGCGTTTGGTGTGTT  
CTTGTCAAGAGTTAGTGAAAATAACTTAGGGAAATTAGTTGAAACATGAGTGGACATTG  
AAAAAACTCAGGCAGCACATTCAAGCAACGCCAGGACAAGCAGGAGTTGCATCTGTCATG  
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAATTCTGCTAAAGATTCTCAATGACTAACCTCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA  
TGCCCTCACGTGAAGTCACTGATGTGGCTGAAATTCTGCTGGGTGTAATTGCTCAAAA  
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGGTGTCCACATCTACAAAGTTAGTCATTCTATAATGACGGCAC  
TAAACTCTGGTACTGAAACAGCTTAAGAAAATGATGAAATGTCGCTGAGCTGGAACCTCAGA  
ACTGTGAGCTAGAGAGAAATCCCACATGCTTTAGCTCAGCTCTCTAATTACAGGAACCTGGAT  
TTAAAGTCCAATAACATTGCAAAATTGAGGAATCATCAGTTCCAGCATTAAACGACT  
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA  
AAAACCTGGAGTCATTATTCCTCTAACACAAGCTGCAATCCTTACAGTGGCAGTATT  
AGTTTACAGAAACTCAGATGTTAGATGTGAGCTAACACAACATTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGCAATACACTGGGAACTGGACATTCTGC  
CAAAACAATTGTTAAATGCAAAAGTTGAGGACTTTGAAATCTGGGACAGAACTGCATCACC  
TCACCTCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGGCCAGTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTGTTG  
TGGAAAGATCACCTTTGATACCCCTGCCACTGAAGTCAGAGGCAATTGAATCAAGACATA  
AAATATTCCCTTGCAAAATGGATTAAACTAAGATAATATATGCAAGTGTGAGTGGCAGGAAC  
AACTTCTAGATTGCAAGTGTACAGTCAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGTAGGGTTTAAAGTCATTCTTCAAAATCATTGTTCTTTGGGG  
AAAGGGAAAGGAAAATTATAACTAACTTGGTTCTTTAAATTGTTGTAACATTGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTGCCACTGAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG  
VPDAVFDLTDLVVLKLELIPAKEAKPAKISQMTNLQELHLCHPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMGLESLRELRLKILHVKSNLTKVPSN  
ITDVAPHLTKLVIHNDGKLLVLNSLKKMMNVAELELQNCELERIPHAIIFSLSNLQELDLKS  
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ  
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRMLKKSGLVEDHLFDTLPLEVKEALNQDINIP  
PANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCACCGCGTCGGCCCTCTCTGGACTTGTGATTCCATTCTTTCACTGACAAACTGACTTTTATTCCTT  
TTTTTTCATCTCTGGCCAGCTGGGATCTAGGGCCCTGGAGACATTGTGTTTACACATAAGGAT  
CTGTGTTGGGGTTCTCTCTCCCTCCCTGGACATTGGCATCTGGCTATGGTTGTTGGGGAGGACCACTGG  
GCTCAGTGTCTGCACTTATCTGCCTAGGATCATCGAACGTTGGACTTACAGTGTATTATGCCCTGTC  
ATCCTGTTGCTATCTGGCCCTGCTCCCTGCTGATATTCTCTGCTCTGCTCTTACTTACAAAATACACAAAC  
GGCTGTTGGGGCAACCCCTTGGAGAGGACTGGGAGAGAACCTCACTGGGAGATCCCTACAGAGCTTC  
CACTGGGGGCAACCCCTTGGAGAGGACTGGGAGAGAACCTCACTGGGAGATCTGGGAGATCCCTACAGAGCTTC  
CACAGCTCTCTTATTCACAAATCTACCCCTTGGCTGGGACTGAGCTTCTCTGGAGGTGTCGAAA  
GCTGATGTAACACAGGCTATAAAAGCTGGCTCTTAAAGGCTGGCTTAAAGGCTGGCTTGGGAAAATGGAGCTTGA  
AGAAGGCTCATGCCATTGACCCCTTAAATCTCTCTGTTGGGGAGCTGACAAATGGGGAGGCTGAGGAAAT  
GCAAGCTGACAGTCAGTCTAGGGGTGCCATATGGCAGAGACCCRAAAGGCAATGATCTGCAACTCAATCCC  
AGTGAAGAATGCACTGGGACATAGAAAAGCAGGAAACAAAGCATCAGAAATTATCTTCTATGTCAGCTT  
GATCAGATGGAAAGCTGTAACAAAGCATTTGAATCATCCAGTACATTGACGGGAAATGCTGAGCTTCTGG  
CAACTGCTGAGTAAACAGACTTGTCTCTGTTGAATCATCCAGTACATTGACGGGAAATGCTGAGCTTCTGG  
GACTCAGCAAAAGTAATCTCTTACTACTCTCTCTCTTCAATCTTCTGAGGCTTAAATAGTTACT  
GGCGGTATCTGGATACCTTGAAGGATCTTCACAGCCCCAATTAACCCAAAGCCGATCTGAGCTGCTTAT  
TGTGTTGGCACAATCAAGTGGAAAGGATACAGATAAAACTAACTCAAAAGAGATTCTTCTAGAAATAGAC  
AAACAGTCAAAATTGTATTCTCTCATCTGATGGCCCTCCACCAACTCTGGCTTGTGAGCTGCTG  
GGCCGTGACTCCACCTTCAAGTCACTAAACACTCTGACTGTGTTGCTACAGATTATGCGCAATTCT  
TACCGGGATTCTCTCATACCTCAATTATGCAAGAAACATCAACATACATCTTAACTTCTCTTCT  
GACAGGATGAGAGTTTATAAGCIAATCTACCTAGAGGCTTTAACTCTAATGGGATAAACTTGCACAACTAAAA  
GACCCAACTTGCAGAAAATTATCAAACTTGTGTTGAAATTCTGCTCTCTTAAATGGATGTGTCACATCAGA  
AAGGTAGAAGATCAGTCATTAACCAATATACTACCTTCTCTGATCTCAACTCTGAGTGTACACC  
CGTCAGAAACAACTCCAGATTATGTGAAGTGTGAATGGGACATATACTCAAGTGGAGATAATACATAACAA  
GAAGATGATGTAATCAAAAGTCAACTGGGAAATATAACACCCAGCATGCTTTTGAATCCAATTCA  
TTGAAAAGACTATACTTGAATCAACCATATTATGTGTTGATTGAAACAAACTCTTGTCAAGTTAGTCTGAC  
ACCTCAGATCAAAATTGGTGTGTTCTGTGATCTGAGCTGAGCCCTTCCACCTCTGACTTGTACATCTCCAAAC  
TACGACCTAATCAAGAGTGGATGTAGTCAGAGTGAACCTGTGAGGTATCCCTTATTTGGACACTATGGAGA  
TTCAGTTAAAGCTTTAAATCTTGTGAAAGTATGAGCTGTGTTCTGCAGTGTAAAGTTTGATATGTGAT  
AGCAGTGCACCACTCTGCTGCAATCAAGGTTGTCTCCAGAACAAAGCAGACATTCTTCTCATATAATGG  
AAAACAGATTCCATAGAGGACCCATTGCTGAAAGGGATGCAAGTGGCAATTTCAGGATTTCAGCAT  
GAAACACATGGGAAGAAACTCCAAACAGGCTTCAACAGTGTGCACTGTTTCTTCTCATGGTTCTAGCTCTG  
AATGTGTTGACTGTAGCAGACATCACAGTGGAGCATTTGTAATCAACGGGAGACTACAAATACAGAGCTG  
CAGAACTTAACTACACAGGCTTCAACCTAAGTGGAGACATGTTCTCAGGATGCCAAAGGAATGCTACCTCGT  
GGCTACACATATTGATAATGAGGAAGGGCTGAAAGTGCACACAGGCCCTGATGTAACAAAAAA

## FIGURE 70

MELVRRLLMPLTLLLILSCLAEIETMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGQVCSKNDYVPVFESSSTLT  
FQIVTDSARIQRTVFVFYFFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKOCKFDFLAIYDGSTNSGLIGQVCGRVTPTFESSSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPCTRP  
KLSNVVEFSPVPLNGCGTIRKVEDQSIYTNTIITFSASSTSEVITRQKQLQIIVKCEMGNST  
VEIYIITEDDVIQSQNALGKYNTSMALFESNSFEKTIILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSVVYL  
QCKVLI CDSSDHQSRCNQGCVSRSKRDIISSYKWKTDISIIGPIRLKDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 71

GACGGAAAGAACAGCGCTCCCGAGGCCGGGAGCCTGAGAGAGGACAGCGGCCCTGCCG  
GGAC**ATG**CGGGCCCCAGGAGCTCCCGCCGTCCCTGCCACAGCGCACCGCCTCGACCCACCTGGAGTCC  
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCCAGTCGGCATCTTCATCCACTG  
GGGAGTGTTCGCCCCAGCTCGAGTGGTCTGGTGGTATTGGCAAAAGGAAA  
AGATACCGAAGTATGCGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT  
TTTGGACCACTATTTACGAAATTTTAATGCCAACATCATGAAGGCTTACCTTGCCCCGT  
CTCTGGTGCCTAACATCATTGCTTAACCTCCAACATCATGAAGGCTTACCTTGCCCCGT  
CAAATATTCTGGAACTGGATGCCATAGATGAGGGGCCAACAGGGACATTGTCAAGGAA  
CTTGAGGTACCCATTGAAACAGAATGCCCTGGTACTGTACTATTCCCTTTGA  
ATGGTTCATCGCTTCCGTGGAGATGAATCCAGTTCACTCCATAAGCGGCAATTCCAG  
TTTCTAAGACATTGCCAGGCTCTAGTGAAGTACTGAACACTATCAGCTGAGGTCTGTGG  
TCGGATGGTGCAGGGAGGACACGGGATCAACTAGGCCAACAGCACAGGCTCTGGCTGGT  
ATATAATGAAAGCCCAGTCCGGGGCAAGTAGTCACTGGTGTAAACCCAGGACATCTTGCA  
TCTGTAAGCTGGTGGCTTCTATACCTGCACTGATCGTTATAACCCAGGACATCTTGCA  
CATAAATGGGAAACTGCACTGACAATAGACAACACTGCTCGGGCTATAGGAGGGAACTGG  
AATCTCTGACTATCTAACATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG  
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCCTGTAGTTTGAG  
GAGCCACTGAGGCAACTGGGCTCTGGCTAAACTGCAATGGAGAAGCTATTATGAAACCTA  
TACCTGGCATCCAGAATGACACTGTCACTGGAGATGTGTGTTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTCTTCTTAAATGGCCACATCAGGACAGCTGTTCTGGCCAT  
CCAAAGCTATTCTGGGGCAACAGAGCTGAAACTACTGGGCCATGGACAGCCACTTAAC  
GATTCTTGGAGCAAATGGCATTATGGTGAAGACTGCCACAGCTAACCATTCATCAGATGC  
CGTGTAAATGGGCTGGCTCTAGCCTAAACTATGTGATC**TAAGT**GCAGCAGACTGGCTG  
ATGTCGAAGTTATGCTAAAGGCTAGGAACATCAGGGTGTATAATTGTAGCACATGGAGA  
AAGCAATGAACTGGATAAGAAAATTATTGGAGTTCAAGGCTTTCCCTTTCCACTA  
AATTTTCTTAAATTACCCATGTAACTTAAACTCTCAGTGCACTTTGCCATTAAAGTC  
TCTTCACATTGATTGTTCCATGTGTACTCAGAGGTGAGAATTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTATTGTGAAGCCATATCCCCATG  
ATTATATAGTTATGCTACTTAATATGGGATATTCTGGGAAATGCATTGCTAGTCAT  
TTTTTTGTGCCAACATCATAGACTGTGTTACAAATCTAGATGCCATAGCTACTACA  
CACCTTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATAACAGCATGTTACTG  
AATACTGTAGGCCAATAGTAAACAGTGTATTGTATATGCAACATATGGAAACATAGAGGAAG  
GTACAGTAAAATTAACACTGTAAATTAATGGTGCACCTGTATAGGGCACTTACCAAGATGGAG  
CTTACAGGACTGGAAGTGTCTGGTGAAGTCACTGTGAGTGAATGTGAAGGCCAG  
TTGAACACTGCCAGACGTTAAATTAACACTGTGTTAGGCTACACTACATTATAAAAAAA  
GTTTTCTTCTCAATTATAAAATTAACATAAGTGTACTGTAACCTTACAAACGTTTAATT  
TTAAAACCTTTGGCTTTGTAAATAACACTTAGCTTAAACATAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPWTESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSFGSEFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAFFNANQWADIFQAS  
GAKYIVLTSKHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHWKENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY  
WRSQNDTVTPDVWYTSKPKELVYIAFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## FIGURE 73

AGCAGGGAAATCCGGATGTCGGTTATGAAGTGGAGCAGTGAATGAGCTCAACATAGT  
TCCAGAACTCTCATCCGGACTAGTTATTGAGCATCTGCCTCTATACCACTGGCCATC  
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCAGGTCTCAGCTGGTGTG  
CTTCTCACTTCATCTGGACACAGGGCTCTGGTCAAAGGCTTTGCGTGAGAAAGAGCT  
TTCATCCAGGTGTCATGCAAGAATTATGGGATCACCCCTGTGAGCAAAAGGGCGAACAGC  
AGCTGAATTTCACAGAAGCTAAGGAGGCTGTAGGCTGCTGGACTAAGTTGGCCGGAAG  
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTGAGCTATGGCTGGTTGGAGA  
TGGATTCTGGTCACTCTAGGATTAGCCAAACCCAAAGTGTGGGAAAATGGGGTGGGTG  
TCCGTATTGGAAAGGGTCCAGTGAGCTTGAGCTTGCAGCTTATGTTACAACATCTGAT  
ACTTGGACTAACCTGTGCAATTGAGAAATTACACCAAAAGATCCATATTCAACACTCA  
AACTGCAACACAAACAGAATTATTGTCAGTGACAGTACACTACTCGGTGGCATCCCCCT  
ACTCTAACATACCTGGCCCTACTACTACTCTCTGGCTCTCCAGCTTCAACTTCTAACCG  
AGAAAAAAATTGATTGTGCAAGAAGTTTATGAAACTAGCACCATGTCACAGAAAC  
TGAACCATTTGGTAAATAAAGCAGCATTAAGAAATGAAGCTGCTGGTTGGAGGTGTC  
CCAGGGCTCTGCTAGTGTCTCTCTTGGTCTGAGCTGGTCTGGATTTGC  
TATGTCAAAAGTATGTCAGGCTTCTTCTTACAAACAAAGAATCAGCAGAAGGAAATGAT  
CGAAAACAAAGTACTAAAGGAGGAGAAGGCAATGATCAGCACCCCTAATGAGGAATCAAAGA  
AAACTGATAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAGAAACTACCGTGCAGTGCCTGGAA  
GCTGAAGTTAGATGAGACAGAATGAGGAGACACACTGGAGCTGGTTCTTCTGCTCC  
TTACCCCTGCCAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAAGAAAGTCCACCCCT  
GGTCTCAACTGGAATCAGCTAGGACTGCCATTGGACTATGGAGTGACCAAAGAGAATGC  
CCCTCTCTTATTGTAACCTGTCGGATCTATCCTCTACCTCAAAGCTTCCACGGCC  
TTCTAGCTGGCTATGTCATAATATCCCAGGGAGAAGGAGTTTGAGGAAAGTGCAA  
GGACCTTAAACATCTCATCAGTATCCAGTGGTAAAGGCCCTCTGGCTGCTGAGGCTAGG  
TGGGTTGAAGGCCAGGAGTCACTGAGACCAAGGCTTCTACTGATTCGAGCTCAGAC  
CTTCTCAGCTGCTGAAGAGAACACGTATCCCACCTGACATGTCCTCTGAGCCGGTA  
AGAGCAAAGAATGGCAGAAAAGTTAGCCCCGTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTGTAAAGCTAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTGTTCTGAAACACATTGAGTTGGA  
ATCAGTGTAGAACACACACTTACTTTCTGGTCTTACACTGCTGATATTCT  
AGGAAATATACCTTACAAGTAACAAAATAAAAACCTTCTATAAAATTCTATTCTATCTGA  
GTTACAGAAATGATTACTAAGGAAGGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA  
ACAAACATTGCTGAATAGCTACTATATGTCAGTGTGCTGCAAGGTATTACACTCTGTAAT  
TGAATATTCTTCTAAAGTCACATAGTAGAACGCTATCTGGAGACTATTCT  
GTTTGATATTCTAGTTACTTCCAAACTAATTCTTATTCTGAGACTAAATCT  
ATTCACTTCTTAATATGGCAACCTTAAACCTTAATTATTAAACATACTTAAAGAAG  
TACATTGTTACCTCTATACCAAGCACAATTAAAAGTGCCATTAAACAAATGTTACACTA  
GCCCTCTTTTCAACAAGAAGGGACTGAGAGATGCCAGAAATTGTCACAAAATTAA  
AGCATTAGAAAACCTT

## **FIGURE 74**

MARCFSLVLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNNPKCGKNGGVVLIWKPVSRQF  
AAVCYNSSDTWTNSCIEIITTKDPIFNTQATQTTEFIVSDSTYVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFVMETSTMSTETEPFVENKAASKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP  
SKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 75

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTGATTGGTGCACGGGACTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTGGCCCTGCTCTGTCGCCCTTCTACTCGTGGAGAA  
ACTGCGCCGCTCTGCCACGGCTGCCACCCAAACGCGAAGACGGTAACCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCTGTGATGTTCTCAGTGCCATTGTGATGATGAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT  
TCTTTCTCCGCTGGATTCGATGGCCACTTTACATCACACTCTGCATGTTCC  
TGATGACGTGCAAACCCCCCTATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACAGAAGGGGACAAGAGGGTCACCTGGATTGGAGTTCTTGCCTA  
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGTCGACCTCCCTTAAATACAAC  
GTACAGGGCTAAATTGGAAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGGGTAC  
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCGTATCCCTGGTCAAGGGCAA  
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTATGGACCTTCTG  
AGGAGAATGTCATCCGAGAATTAACTTAAATGAGCTATACCAGGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACACAGTGTCA  
TGGGGAAAACAAGAAGGATAATAAGATCTCACTTGGCAGTGTCTCCCTGTCAATT  
CCAGGCTCTTCCATAACCAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG  
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTAAAGAGGCATCTAGGGATTGTCAG  
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCAACTGTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTGGGTCACTGTGTTAACGTCTTATC  
AGCTATTCAAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTCTTAG  
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA  
CGCTAAGAATTCCCTCAAGGACTCTGCTTCTTAAGCCCTCTGGCTTCGTTATGGTC  
TTCAATTAAAGTATAAGCCTAACTTGTGCTAGTCCTAAAGGAGAAACCTTAAACCAAAG  
TTTTATCATGAAGACAATTGAACACCCCTATTGGTGGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTCCCTTGTGTTAGGACTGGAGGAGAAACCCCTGGACTTCA  
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAAATAAAAGATTGGATT  
TCCTTTG

## **FIGURE 76**

MAVLAPLIALVYSPVRLSRWLAQPYYLLSALLSAAFLLVRKLPPCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTI DEELERDKRVTWIVEFFANWSNDCQSF APIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKSKAGDNIPPEQPVASTPTTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## **FIGURE 77**

GGACAGCTCGGGCCCCGAGAGCTAGCCGTCGAGGAGCTGCCCTGGGACGTTGCCCTG  
GGGCCCCAGCCTGGCCGGGTCACCCCTGGCATGAGGAGATGGCCTGTCCTGGTCCA  
TTGCTCCCTGCTGCCGGCTCCAGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG  
CGCCAACGACAGAACCTAGGCAACGGTCATGGCAAAGACCTCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGAGACCCGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCGCGCGTGTGCGTGTCAAATGGTGAAGCT  
GTGCGAGAACGGGGCCCCAGAGAAGGACGTCGTGGTGGCATCGGCTGAGGCACCGCTCCT  
TTGGGGACTACCAAGGCCGCGTGCACCTGGCGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTCGCCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGGCTGGA  
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTCCTTACAGTCCCCA  
ACGGGGCTACAGTCACCTTCACGAGGGCCAGCAGGTCTGTGAGAGCAGGCTGCCGTG  
GTGGCCTCTTGTAGCAGCTTCCGGGCTGGAGGGGGCTGGACTGGTGAACCGGG  
CTGGCTGCAGGATGCTACGGTCAGTACCCCATCATGTTGCCCGGAGCCCTGCGTGGCC  
CAGGCCCTGGCACCTGGCGTGCAGAGCTACGGCCCCGCCACCGCCGCTGCACCGTATGAT  
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGTGACTACCTGGAGCACCTGAGAACCT  
GACGCTGACAGAGGAAGGGAGGCTGCCAGGAAGATGATGCCACGATGCCAAGGTTGGAC  
AGCTTTGCGCCCTGGAAGTTCATGGCTGGACCGCTGCGACGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCCTGTGGTACCCGATCCTAACTGTGGGCCCCAGAGCCTGGGT  
CCGAAGCTTGCTCCCCGACCCGAGAGCGCTGTACGGTGTTACTGCTACCGCCAGC  
ACTAGGACCTGGGGCCCTCCCTGCCGATCCCTCACTGGCTGTGTTTATTGAGTGGTT  
CGTTTCCCTGTGGGTTGGAGGCATTTAACTGTTTATCTCTCAATTAAATTCT  
TTAACATTTTTACTATTTTTGTAAAGCAAACAGAACCCAAATGCCCTCCCTTGCTCTG  
GATGCCCACTCCAGGAATCATGCTGCCCTGGCATTGCGGTTTGCGGCTTCTG  
GAGGGTTCCCGCCATCCAGGCTGGTCTCCCTCCCTAAAGGAGGTGGCAGAGTGGG  
GGTGGCCCTGCTAGAATGCCCGGGAGTCGGGAGTCGGGAGTCGGCTTGGGCTCTGCC  
CAGCCCTGGGGAAAGAAGGGCTCGGGGCTCCGGAGCTGGGCTTGGGCTCTGCC  
CACCTCTACTTCTGTGAAGCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGAA  
GCCAGTTCTAGGCTCCAGGGAAATCTGAGGGAGGAAGAAACTCCCCCTCCCGTTCCCT  
TCCCTCTCGGTTCAAAGAATCTGTTGTGTCATTGTTCTCTGTTCCCTGTGTTGG  
GGAGGGGCCCTCAGGTGTGACTTTGGACAATAAATGGTGTGCTATGACTGCCCTGGCAA  
AA  
AA

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYNSNSANDQNLGNHGKDLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRLLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPPVPHPMCGPPEPGVRSGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**AT**GATGTGGCGACCACATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCAGACGCCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAGCGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA  
CTTCCAGTACGACCATGAGGCTTCTGGACGGGAAGTGGCAAGGAATTGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCGTCTGGGGCGATCGTGACCGCATGGACCGCGGGGGAC  
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGCGTGATCGGCACACGCAAGCAGCGGA  
CATACGGGACTCGGTGAGCGCGGCCCTGGACACGTACGACACGGACCCGACGGCGTGTGG  
GTTGGGAGGGAGCTGCGCAACGCCACCTATGGCACTACCGGCCGGTGAGAATTGATGAC  
GTGGAGGATGAGAGACCTACAAAAGATGCTGGCTGGGACGAGCGCGTTTCCGGTGGC  
CGACCCAGGATGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTGCACCCCGAGG  
AGTTCCCTCACATGGGGACATCGTATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCAGGTGGAGGAGTACATCGGGATCTGTA  
CTCAGCCGAGCCTGGGAGGA  
GGAGCCGGCGTGGGTGAGACGGAGGGCAGCAGTTCCGGACTTCCGGATCTGAACAAAGG  
ATGGGCACCTGGATGGGAGTGGGTGGCCACTGGGTGCTGCCCTGCCAGGACAGCCC  
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGCAAGGATGGCGGCTGAGCAA  
AGCGGAAATCTGGTAATTGGAACATGTTTGTTGAGCTGAGCACCACGCCACAGCCTCAGAGGCCG  
ACCTGACCCGGCACCACGATGAGCTG**TGAG**CACCGCACCACGCCACAGCCTCAGAGGCCG  
ACAATGACGGAGGAGGGGGCGCTGTGGTCTGGCCCTCCCTGTCCAGGGCCCGCAGGAG  
GCAGATGCAGTCCCAAGGCATCCTCTGCCCTGGCTCTCAGGGACCCCTGGGTGGCTTC  
TGTCCTCTGTCACACCCCCAACCCCAGGGAGGGCTGTCTAGTCCAGAGGATAAGCAATAC  
CTATTTCTGACTGAGTCTCCCAAGCCAGACCCAGGGACCTTGGCCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACACATAGACTGAAACTCCCT  
GGCCCCAGCCCTCTGCTGGCTGGCTGGACACCTCCTCTGCCAGGAGGAATAA  
AAGCCAGCGCCGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFQFDQLTPPEESQARLGRIVDRMDRAGDGDWVSLAELRAWIAHTQQRHIRDVSAAWDT  
YDTDRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ  
FRDFRDLNKGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## FIGURE 81

GGGGCCCTTGCCTTCCGCACTCGGGCGCAGGGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GCGGCGGGCGGGGTGCGAGGGATCCCTGACGCCCTGTCCTGTCCTTCTTGTGCTCCAG  
CCTGTCGTCGCTCGTTTGGCGCCCCCGCTCCCGCGGTGCGGGGTTGACACCCGATCCCTG  
GCCTTCGCTCGATTTCGCCCGAGGGCGCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
CGGGTCTGCTGTGTCCTCTCCTCTCGCCGGCGCCGGGGATCCGAAGGGGTGCGGGGCTCT  
GAGGAGGTGACCGCGGGGCGCTCCCGCACCCCTGCGCTTGCCGCATTCTCCCTCTCTCCAG  
GTGTGAGCACCTATCAGTACCATATGTCCGAGCCTGGATCCGGCTCGGCTCGGTGTG  
TGTCGCTGCTGCTGCGCCGGGGCCCGGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG  
TTTACAGGGCTTGGACATCAGGAAAGAGAAGCAGATGTCCTCTGCCAGGGGCTGCC  
CTCTTACAGGGAACTCTGTGATGGGACATAGTATGCTTCTGTATCGAGCATATGTGGG  
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACAGTCTATAGCCTACC  
TGTCGAGAAAACATTCTCAGTAGATGGCAATCCAGTCTCAAATGCTTTCTAGAT  
GGTCGCTCTTACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCACCAACAGTAAAGCAGTAAAGGAAACACCCAGAAGAAAATGG  
CAATAAAGATTGTAAGCAGACATTGCAATTCTGATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTAAATTACAGAAGAATTGTTGGGAAAGTGGCTTAATGTTGGGAATTGGAAACA  
GAGGACCCACATGTGGGCTTGTCAAGCCAGTGAACATCCCCAAATAGAATTTCAGTGA  
AAACTTACATCAGCCAAAGATGTTTGTGCTTGCATAAAGGAAGTAGGTTCAAGGGGGTA  
ATTCACATCAGGAAAGCCTGAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA  
GTAGAAAAGGGATCCCCAAAGCTGGTGTGTTATTATTGATGGTTGGCCTTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTCAATGTATTAGTTCTGTGGCCA  
AGCCTATCCCTGAAGAACCTGGGGATGTTCAAGGATGTCACATTGTTGACAAGGCTGCTGT  
CGGAATAATGGCTCTCTCTTACACATGCCAACACTGGTTGGCACCACAAAATAGTAAA  
GCCCTGTTGACAGAACGACTGCACTGATGAACAAATGATGTCAGAACACTGTTAAACT  
CAGTGAACATTGCTTCTTAATTGATGGCTCCAGCAGTGTGGAGATGCAATTCCGCCTC  
ATGCTGTAATTGTTCCACATGCCAACACTGGGAACTTCTGGACATTGGTCCAGAAGAT  
AGCTGCTGTAAGTTTACTTATGATCAGGCCAGGGAGTTCAAGTTCACTGACTATAGCACC  
AAGAGAATGTCCTAGTGTCACTAGAAACATCGCTATAGTGGTGGAACAGCTACTGGT  
GATGCCATTCTCTTCACTGTTAGAAATGTTGGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCTCTAGTAATTGTCAGAGATGGGCACTTATGATGTCAGGCCCTGAGCTGCTG  
CACATGATGCCAGGAATCACTATCTTCTGTTGGTGTGCTGGCACCTCTGGATGACCTG  
AAAGATATGCTCTAAACCGAAGGAGTCTCACGCTTCTTCAAGAGAGTTCAAGGATT  
AGAACCAATTGTTCTGATGTCATCAGAGGCAATTGAGAGATTCTAGAATCCAGCAAT  
ATGGTAACATTGACAACCTGAAAGAAAAGTACAAGGGATCCAGTGTAAATTGTTATT  
CTCATAAATCTGAAATGCTTAGCATACTAGAATCAGATAACAAACTATTAAAGTATGTCAC  
AGCCATTAGGAAATAAGCACTCTTAAAGCCGCTGCCCTCTGGTACAATTACAGTGT  
ACTTTGTTAAAACACTGCTGAGGGCTTCAATCATGGCTCTTAGAAAACCTCAGGAAAGAGGA  
GATAATGTCGATTAAAACCTTAAGAGTTCAACCTGCTACTAAATGTCAGATATGCAAA  
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAA

## **FIGURE 82**

MSAAWI PALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEADVLCPGGCPLEEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCDIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAlKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNGFFSYHMPNWFGSTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIACFLI  
DGSSSGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLA  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVITDQGSYDDVQGPAAAHDAGITI  
PSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

### **FIGURE 83**

CGCCCGCGCTCCCGCACCGCGGGCCGCCACCGCGCCGCTCCCGCATCTGACCCCGAGCCC  
GGCGGCCCTCCGGCGGGAGCAGCGAGCATCTCAGTCAGGCCGCCGAGCAGCAACTCGGTCAGTCG  
GGCGGCCGCGCTCGGGCGCACAGGGAGATCGAGCGCTTGGGGCACCTCTGCTGCGCT  
TGCTGGCGCGGGCGTCCCCACGGCCCCCGGCCGCTCGAGCGCACCTCGGCTCAGTC  
AAGCCCGGCCGGCTCTCAGCTACCCGAGGAGGGCACCTCAATGAGATGTTCCCGA  
GGTTGAGGAAGACTGTGGAGCACCGAGCACAAATTGCGCAGCGGGCTGGAAGAGTGAGG  
CAGAAGAACGACTGCTGCTAAAGCATCATCAGAAGTGAACTGGGAAACTTACCTCCGAGCTTAT  
CACAATGAGACCAACACAGACAGAAGGTTGGAAATAATACCATCCTAGTGCACCGAGAAAT  
TCACAAGATAACCAACACAGACTGGACAATGGCTTTTCAAGAGACAGTTACATCATCTG  
TGGGAGCAGAAGAAGGAGCAGAAGGAGCCAGTGCATCATCGACAGGAGACTGTGGCCAGC  
ATGTAECTCCAGTTTGCAGCTTCACTGAGACCTCCAGTACACCTGCAGCGCACATCGGGGGCAAGAGGATGCT  
CTGCACCCGGACAGTGAGTGTGGAGACCGAGCTGTGTCTGGGGTCACTGCACCAAAA  
TGGGCCACCGGGAGCAGATAAGGACCATCTGTGACAAACAGGGAGCTGCCAGGGGGCTG  
TGCTGTGCTTCCAGAGGGCTCTGTTCTGTGTCACACCTGCCTGGGGCTGGAGGCGA  
GCTTGGCATGACCCCGCAGCGGCTCTGGACCTCATCACCTGGAGCTAGAGCTGTAG  
GAGCCTGGAGCCTGGAGCTTGTGCAAGTGGCCTCTCTGGCACAGCCACAGCTG  
GAGCCTGGAGCCTGGAGCTTGTGCAAGTGGCCTCTCTGGCACAGCCACAGCTG  
GTGTATGTGTCAGCCGACCTTCCTGGAGGACCTGACAGAAGGAGACTCTGTGCG  
CAGAGAGGTTCCCGATGAGTATGAAGTGTGGCAGCTTACAGGAGGGTGCAGCAGCTGG  
AGGACCTGGAGAGGAGCTGACTGAAGAGATGGCGTGGGGAGCTGCGCTGCCCGCT  
GCACACTGCTGGAGGGAGAGATTTAGATCTGGACCCAGCTGTGGTAGATGTGCAATAGAA  
ATAGATAATTATTTCCTCCAGGTGTGCTTGGCTGGGTGACACAGGCTTCTTCA  
TCTTCTCCAGTAAGTTCCTCTGGCTTGACAGCATGAGGTGTGCAATTGTCAGC  
TCCCTCCAGGTGTTCTCAGGCTTCACAGTCTGGTCTTGGAGAGTCAGGCAGGGTTAAC  
TGCAAGAGCAGTTGGCAGCCCTGTCAGGATTATGGCTGCTTGTCTCTACAGTGGCAG  
ACAGCGCTTGTCTCATGAGCTTGTGATAATTGTTGAGGGAGGAGATGAAACATGTG  
AGTCTCCCTGTATTGGTTTGGGAAATGTGGAGAGAGTGCCTGCTTGTCAAAACATCAA  
CTGGCAGAAATGCAACAAATGAATTTCAGCAGCTTCTTCCATGGCATAGGGTAAGCTG  
TGCTCTCAGGTGTCAGATGAAATTGTTCTGGTCTTGGCTGACACAGGCTTCTGGC  
AGCAGTGTGTCAGCTCTACCTCTGGCAGGGCAGCATTTCATATCCAAGATCAATT  
CCTCTCTCAGCACAGCCTGGGGAGGGCTATTGTTCTCTGTCAGGATCTCAGAG  
GTCAGACAGACTGCAAGCTGCTGGCCAACTACACAGCTAGTGAAGACAGAGCAGT  
CTGGTGTGACTCTAACGCTAGTGCCTCTCCACTACCCACACAGCTTGGTGGC  
AAAGTGTCTCCCAAAAGGAAGGAGAATGGGATTTTCTGTGGAGCATGACATCTGG  
GTCAAAACTATTCTCACCTCTAAAGTAACACTGTGAGGAGACAGCAGTGTCTC  
AGTGTGGGGCAGCGCTCTTCTAATGAAGAACATGATATTGACACTGTCCTCTGGAGT  
TGCATTAGTAACATTGAAAGGTATATGACTGAGCGTAGCATAAGGTTAACCTGCAAGAAC  
GTACTAGGTAAATTGTAGGGCAGGAGTATAAAATGAAGATTGTCAGGAAACATCTAGGAGC  
TGAAGAACATTATCACACCGTCAGGAAATAACCCAGCAGGGCTGTGCAACATGGT  
GTAATATGCGACTGCGAACACTGAACACTACGCCCCACTCCACAAATGATGTTTCA  
TGGACTGTGGCCACATGTATTGATCCAGAGTTCCTAAGTTAAAGTTAAAGTGCACATGATTGTA  
TAAGCATGCTTCTTGTGAGTTTAAATGATGATAAAACATAAGTGTGCAATTAGA  
ATAAAATCCTCACTGCAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 84**

MQLRGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDKVGNNTIHVRREIHKITNNQTG  
QMVFSETVITSGDEEGRRSHECI IDEDCGPMYCFQASFQYTCQPCRGQRMLCTRSECCG  
DQLCVWGHCTKMATRGNSNGTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPGASGLLCQPHSHSLVYCKPTFVGSRDQDGIEILLPREVPDEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGGEET

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 85**

## **FIGURE 86**

MRLLVAPLLLAWVAGATATVPVPPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLQSNIVRVDQSELGYLANLTEDLSQNSFSDARCDFHALPQLLSSLH  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLSLAGMNLRREISDYALEGLQSLSESLSFYDNQ  
LARVPRRALEQVPGKFLDLNKNPLQRVGPQDFANMLHILKEGLLNNMEEELVSIDKFLAVNLP  
ELTKLDITNNPRLSFIHPRAFHHPQMETLMLNNNALSALHQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLO  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRGRVYPEGTIELRRVTAAEAGLYT  
CVAQNLVGDATKTVSVVVGRALLQPGRDEGGCLELRVQETHPYHILLSWVTPPNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLTIALALAVLLAAGLAAHLLGTGQPRKGVGRRPLPPAWAFWGSAPSVRVV  
SAPLVLWPWNPGRKLPRSSSEGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## **FIGURE 87**

## FIGURE 88

MRQTI IKVIKFILII CYTVYYVHN IKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSIDIPDVKNDFAPFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQQLNNEWTLDKLRLQRLTKNAQDKLELHLFMLS GIPDTVFDLVELEV  
LKLELIPDVТИPPSIAQLTGLKELWLWYHTAAKIEAPALAFLRENRLRALHIKFTDIKEIPLWI  
YSLKLTLEELHLTGNLSEAENNRIVIDGLRELKRLKVLRLKSNSKLPQVVTDVGVLQHQLKLSI  
NNEGTKLIVLNSLKKMANLTELLELIRCDLERIPH SIFS LHN LQEIDLKDNNLKTIEIIISFQ  
HLHRLTCLKLWYNHIA YIPIQIGNLTNLERLYLNRN KIEKIP TQLF YCRKLRYLDDSHNNL T  
FLPADIGL LQNLQNLAITANRIETLPPPELFQCRKLRLAHLGNNV LQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECP PLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCCGTACTTGTCAATGGAGCTGGCACTGCCGCGCTCTCCCGT  
CCCGCGGTGGTGCTGCTGCCGTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT  
GGCCACAGAGGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCATACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGGCGTTCTAGCACTGGATTGGAAACTTTGAGGAAATTGGGC  
CCCTTGACAGTGTACTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGACTGGGTTCACTGGGTTCACTGGGTTCTCTGAAGACCTTCAGTTGCCAACAGA  
CCTGGCTATGGTGGCTTCAGACATGATGGGTTCTCTGAAGACCTTCAGTTGCCAACAAAG  
AATTCCAGACAGTCCATTCTACATTTCCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTATAAGGCCATTAGCAGGGACCATCAAGTGCACATTGCGGGGGT  
TGCTTGGGTGATTCTGGATCTCCCTGTTGATTGGTCTCTCTGGGACCTTACCTGT  
ACAGCATGTCCTCTCGAACAGAACAGGCTGGCAGAGGTGTCTAAGGGTGCAGAGCAAGTA  
CTGAATGCCGTAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGGTGAACTTCTATAACATCTTAACTAAAGCACTCCCA  
CGCTACAATGGAGTCGAGCTAGAATTCAACAGAGCCACCTAGTTGCTTTGTCAAGC  
CACGTTGAGACACCTACAACAGAGATGCCCTAACGCCAGCTCATGAATGCCCATCAGAAAAGAA  
GCTCAAATTATTCCTGGAGGATCAATCTGGGGAGGCCAGGCTACCAACGTCCTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTTGACGGGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCCTG  
GGTGGGAAACTGAAGTGGCCAGAACACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT  
ACAGTGACCTAAATCTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGTCTTC  
TACTGGATTCTGAAAGCTGGTCATATGGTCTCTGACCAAGGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGAECTCAGCAAGAAAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT  
TGGGGCAAGAGCTGAGCTGAGGCCGCTGAAGCTGAGGAAGCGCCATTCTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGACAGAGGATAAAATCATTGCTCT  
GGAGGCAATTGGAAATTATTCCTGCTCTTAAAAAAACCTAAGATTTTAAAAAATTGAT  
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEIIGPLDSLKPRKTTWLQAAISLLFVDNPVGTFGSY  
VNGSGAYAKDLMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTLKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGGLAEVSKVAEQVLFNAVNGKGLYRE  
ATELGKAEMIIEQNTDGVNFYNIITKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEANVRKLKWPELEPKFSQLKWALKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## FIGURE 91

GGCCGGGGAGAGGAGGCCATGGGCGCGCGGGGGCGCTGCTGCTGGCGCTGCTGGCTCG  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCAGTCGCGCATCGTGGGTGGAGAGGACGCCAACTCGGGCGTTGGCGTGGCA  
GGGGAGCCTGCCGTGGGATTCCACGTATCGGGAGTCAGGCCACTCGGCCACCGCTGGG  
CACTCACGGCGCGCACTCGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGGCCCGCTACCTGGGAATTCAACCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTACCTAACACATCCAGCCATCTGCTCCAG  
GCCTCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCACCCCTCCAGGAAGTTCAGGTGCCATCAAACA  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGAAGGACATCTTGGAGACATG  
GTTTGTCTGGCAACGCCAAGGGGGAGGATGCCCTGCTTCGGTGACTCAGGTGGACCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGGCCAATCGGCCGGTGTACCCAATATCAGCCACCACTGGAGTGGATCCAGAAG  
CTGATGGCCAAGGTGGCATGCCAGCCAGACCCCTGGCCACTACTCTTTCCCTCT  
TCTCTGGCTCTCCACCTCTGGGCCGGTTGAGCCACTTGAGCCATGCAGCCTGGGC  
CACTGCCAAGTCAGGCCGTGGTCTTCTGCTTGGTAATAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLALLARAGLRKPEAAPLSGPCGRRVITSRIVGGEDAEELGRWPWQGSLRLW  
DSHVCVGVSLLSHRWALTAACFETYSDLSPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLsapVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSVGVCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## **FIGURE 93**

CCCCACGCGTCCGGCGACGGCTGGGAAGGGCAGA**ATGGGACTCCAAGGCTGCCCTCTAGGGCT**  
CTTGGCCCTCATCTCTCTGGCAAATGAGCTTACGGCCGGAGGCCACAGCGGAGGAGCC  
TGCCCCCAGGGCTGGGGCTCCCTGGGCGGACCTGGAGGAAGAGCTGACCTCACCTT  
GCCCTGAGACAGCAGAAATGTGAAAGACTCTCGGAGCTGGTGCAGGGCTGTGCGATCCCAG  
CTCTCTCATACGGAAAATACCTGACCCTAGAGAAATGTGGCTGATCTGGTGGGGCATCCC  
CACTGACCCCTCCACAGCGTGAAGGAAATGGCTCTGGCAGGGAGGCCAGAAGTGGCCATTCT  
TGATGACACAGGACTTCTGACTCTGGCTGAGCATCGAACAGAGCTGCTGCTGCC  
TGGGGCTGAGTTTCACTACTATGTGGGAGGACCTACGGGAAACCCATGGTGAAGTCCCCAC  
ATCCCCTACCGCTTCCACAGGCCCTGGGCCCCCATGGACTTGTGACTTGTGGGGGACTGACCGT  
TTCCCCCAACAGCATCTCTGGAGGCAAACCTGCTGAGGCCGAGGTGACAGGGACTGTAGGG  
GCATCTGGGGTAACCCCTCTGATCTGCTGAGCATACATCTGGACCTCAACAGAGCTGG  
GCTCTGGCACCAGCAATAACAGCCAAGGCTGTGCCAGTCTGGAGCAGTATTTCCATGAC  
TCAGACCTGGCTGACTTCTGCGCTCTCGGTGCACTTTGACATCAGGACATCAGTAGC  
CCGTGTTGGTGGACAACAGGGCCGGGGGGGGGGGGATTGGAGGCCAGTCTAGATGTGCACT  
ACCTGATGAGTGTGCTGCTGCAACATCTCACCCTGGTCTACAGTACGGCTGGCCGAG  
GGACAGGAGGCCCTCTGCACTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGACTCTCTGAGCAGGGCTACATCCAGGGTCA  
ACACTGAGCTCATGAGGCTCGGGCTCTCCGGTCTACCTCTGCTCTGGCTCAGGTGAGC  
GGGGCCGGGTGTTGGTCTGCTCTGGAGACACCACTGGCCCTACCTTCTCTGGCTCC  
CCCCCTATGTCACCAACAGTGGGAGGCAACATCCCTCCAGAACCTTCTCATCACAAATGAAA  
TTGTTGACTATATCAGTGGTGGCTTCTGCAATGTGTTTCCACGGCCATCAGGAG  
GAAGCTGTAACGAAGTCTCTGAGCTCATGCCACCTTCCAGTACTTCAATG  
CAGTGGCGTGCCTACCCAGATGTGGCTGACTTCTGATGGCTACTGGTGGTCA  
GAGTGGCCCATTCCTGGTGGCTCCGGAACTCTGGCCCTCTACTCTCAGTGTGGGGGATCTA  
TCTCTGTGATCAATGAGCACAGGATCTTCTGGCCGGCCCCCTCTGGCTTCTCACCCAAAG  
GCTCTACCAAGCAGCATGGGGCAGGTCTCTGGTACTGATCTAACCCCTGGCTGC  
TGGGATGAAGAGGTAGAGGGCCAGGGTCTGCTCTGGCTGGATCTGTAACAGGC  
TGGGGACACCAACTTCCACGGCTCT**TGAAGACTCTACTCACCCCTGACCTTCTCATC**  
AGGAGAGATGGCTTCTGCCCTGGCAAGCTGGCAGTCTCAGTCTCTTATTCTGCCCTGTG  
GAAGGCCCTGCTGAACCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCGTAAA  
TGCTGTGAGCTTACTGACTCCAAACCTTCTGCTCCATCATACTCAGGTCTCC  
CTGGCTTCTGGATCTTCTCAATAGATGCTGTAACAGTATTTTGATGCTCTCC  
ATCTCATCTTCTCTTCACTCAGGCTTCTCAAAAGGGTTGATACAGACTCTGTGACTA  
TTCACTGTGATATTCTTCTACCTCCAAATTCACTGCAAGGGACCTCTACTGTCACCGTTACTCT  
TCCCTACCCCTGACATCCGGAAACAACTGGCTCTGGCTGACATCTCTCATCTTGTGTTTATG  
GCCCTTCTCATCATAGTGGCCACTCTCTCTTACTGCTCTGGAGGCTTCAACTCTCTG  
ACTACTCTGTCTTCTCTCATCAATTCTGCTCTCATGGAATGTCGACCTTCAATTG  
TCCATTGAGATTGGCTCTCATGTTACTCATGGTCCCTGGAAACAAATCACTGAC  
TCTACAAACCTTACCATCTCACTAAAGACTTCTATCCAATAATGATTGATACTCTCAAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLAAAGAQKCHSVITQDFLTCWL  
SIRQAELLLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGLHRFPPSSLRQRP  
EPQVTTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDEDSILSSAYIQRVNTELMKAAARGLTLFASGDGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGSNFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNSRVPIPWVSGTSASTPVFGILSLINEHRLSG  
RPLGLFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## FIGURE 95

GGCGCGCGCTCTCCGGCGCCACACCTGCTGAGGGCGCAGCGAGCCGCGCCGGC  
GGGCTGCTCGCGCGGAACAGTGCCTGGC**ATGGCAGGGATTCCAGGGCTCTTCTTCTC**  
**TTCTTCTGCTCTGTGCTTGGCAAGTGA**GGCCCTAAGTGCCTGGAAACCACTTG  
GCCTGCATAACGCCCTCCGTGCTTGCCTAGCTACCCCTCAATTAGCCAAGCCAGACT  
TTGGAGCGAAGCCAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTATGAAACGCTATGCCAATGG  
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG  
CAGCCGACAGAGACGCAAGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC  
ACCGAGACTCAGGGTCTCAGGAAAGTCTGAAGGAAGCGCAGATTATGGCTATGACAGC  
AGGTTCAAGCATTTGGAAAGGACTCTGCTCAACTACCCCTTCACACATCAGTGAAGTT  
ATCCACGGGCTGCACCGCACCCCTGGCAGAGAACGATGCTCACAGCTGCCACTGCA  
TACACGATGAAAAACCTATGTGAAGGAACCCAGAACGCTTCAGTGCTTCTAAAGCCC  
AAGTTTAAAGATGGTGGTCAAGGGCCAACGACTCCACTCAGCCATGCCAGCAGATGAA  
ATTCAGTGGATCCGGTGAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCTGAACTCAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGTGAGGCCCTCTGCTAAGCAGCTGCCAGGGGAGAATTCACTTCTC  
TGGTTATGACAATGACCGACAGCAATTGGTGTATGCCCTCTGTCAGTCAAAGACGAGA  
CCTATGACTGCTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGCGGTCTGGGTCTAT  
GTGAGGATGTGAAAGAGACAGCAGCAGAACGTTCAACGTGGCTGTCAAATCACTC  
CTCTCAAATATGCCAGATTGCTATTGATTAAAGGAAACTACCTGGATTGTAGGGAGGG  
**TGACACAGTGTCCCTCTGGCAGCAATTAAAGGTCTCTCATGTTCTTATTAGGAGAGGC**  
AAATTGTTTGTCTATTGCTATTGGCTGCACAGTGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAACTG  
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAAACTGATTGGGCAATGAGGAATTGGACAATTAAAGTTAATCTCACGTTTG  
CAAACATTGATTTCATCTGAACATTGTTCAAGATTATTAATTAATTTGGCATA  
CAAGAGATATGAAAAAAAAAAAAAA

## **FIGURE 96**

MAGIPGLLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNIAKPDFGAEAKLEVS  
SSCGPQCHKGTPYEEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRDGSQGKSS  
RRKRQIYGYDYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAACIHDGKTYVKG  
TQKLRVGFLKPKFDGGRGANDSTSAMPQMKFQWIRVKRTHVPKGWIKGNNANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLYQQCD  
AQPGASGSGVYVVRMWKRQQQKWERKIIGIFSGHQVDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## **FIGURE 97**

GCATGCCCTGGTCTCTGAGCCTGCTGCCCTGCTCCCCGCCCCACCAGCC**ATGGTGGTT**  
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCCTCGGCACCTTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTCAGGCTGTGGGAAGCCCA  
GCAGCTGAACCGGGTGTGGCGAGGACAGCAGCTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACACTGCGCAGGTTCTGCTCACAGCCGCTGGGTGATC  
ACTGCTGCCCACTGTTCAAGGACAACCTGAAACAAACCATACCTGTTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCTGGCTCTGGTCCCAGAAGGTGGGTGTGCTGGTGGAGC  
CCCACCTGTGTATTCTGGAAAGGAAGGTGCTGTGCAGACATTGCCCTGGTGCGTCTCGAG  
CGCTCCATACAGTTCTCAGAGGGTCTGCCCATCTGCTACCTGATGCCCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC  
CCCACCCCTCAGACCCCTGAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTAAGGGGGAGGGGAGCTGGGATGTTCTGGGCGACTCCGGGGGCCCTCATGTGCCAGGTGGACG  
GCCCTGGCTGCTGGCCGGCATCATCGCTGGGGCAGGGCTGTGCCGAGCGAACAGGCC  
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGGTGGAGAAGATCGTCAAGGGGTGCA  
GCTCCGCGGGCGCCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCG  
CCGCCTGCTCC**TAGGGCGCAGCGGACGCGGGCTCGGATCTGAAAGGGGGCCAGATCCACA**  
TCTGGATCTGGATCTGGCGCCCTGGGGGTTCCCCCGCTAAATAGGCTCATCTACC  
TCTACCTCTGGGGCCCGAACGGCTGCGGAAAGGAAACCCCTCCCGACCCGCCGAC  
GCCCTCAGGCCCGCCCTCCAAGGCATCAGGCCCGCCAACGGCTCATGTCGGGCCCGAC  
GACTTCCGGCCCGCCCCGGGGCCAGCGCTTTGTGTATATAATGTTAATGATTATT  
AGGTATTGTAAACCTGCCACATATCTTATTCTCCAATTCAATAATTATT  
CTCCAAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
M V V S G A P P A L G G G C L G T F T S L L L A S T A I L N A A R I P V P P A C G K P Q Q L N R V V G G E D S T D S E W P  
W I V S I Q K N G T H H C A G S L L T S R W V I T A A H C F K D N L N K P Y L F S V L L G A W Q L G N P G S R S Q K V G V A  
W V E P H P V Y S W K E G A C A D I A L V R L E R S I Q F S E R V L P I C L P D A S I H L P P N T H C W I S G W G S I Q D G  
V P L P H P Q T L Q K L K V P I I D S E V C S H L Y W R G A G Q G P I T E D M L C A G Y L E G E R D A C L G D S G G P L M C  
Q V D G A W L L A G I I S W G E G C A E R N R P G V Y I S L S A H R S W V E K I V Q G V Q L R G R A Q G G G A L R A P S Q G  
S G A A R S

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGGCACCAATGCACGGCTCTGCAGTTCTGATGTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCACCAACGGCCCGTTGGAGGCCACAGATGAGGAGAAACGTTGATGGT  
GGAGCTGCACAAACCTCTACCGGCCAGGTATCCCGACGCCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCCTCGCAAGGCCAACGGCTACGCAGGCTGTCGTGGGCCAC  
AACAAAGGAGCCGGCGCCGGCGAGAAATCTGTCGCACACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACACAGCGTGAAGCACTACAAACCTCAGGCCGCCACCT  
GCAGGCCAGGCCAGATGTGGGCCACTACACGAGGTGGTATGGGCCAGACAGAGGGATC  
GGCTGTGGTCCCACCTCTGTGAGAAGCTCAGGGTTGAGGAGACCAACATGAAATTACT  
GGTGTGCAACTATGAGCCTCGGGGACGTGAAGGGAAACGCCCTACAGGAGGGACTC  
CGTGCCTCCAAATGTCCTCTGGCTACCAACTGCAAGAACCTCTGTGAACCCATCGGAAGC  
CCGGAAAGATGTCAGGATTGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTTCT  
TGGTAAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTGCTGCTGAGGAAACCCAGGCC  
CCAACCTCTTAGCAACGAAAGACCCGCCCTCATGGCAACAGAGGCTCACCTTGTAAAC  
AACTGAGGTCCCTCCATTGGCAGTCACAGCCTGCCCTCTGGATGAGGAGCCAGTTA  
CTTCCCCAAATGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCTCTAGGAGCCAGAGAACTCTCTGGACCCAAAGATGTCCCTGACAGGGCAAG  
GGAACCTCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCTCTTCCAGTG  
AGGTCTTGGCTCAGTTTCCAGGCCAGACAAGGCCAGGTGAGCTGAGGCCACACTGGAC  
CACACGGGCCACACCTCTCCAAGTCCTGCCAATTTCCAAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTCTGCACTCGTCTGCAAGGTGAGGCCCTTGACA  
AGCCTAGCGTTGTCAAGGGCTGAACTCGGGCCCTGGTATGTGAGGGCCCTCTGGGA  
CTACTGCTCTGCCCTCTGGTGTGGCTGGAATCTTGAATGGGATACCACCTCAAGGG  
TGAAGAGGTCACTGTCCTCTGTCATCTCCCCACCCCTGCCCCAGCCCTAAACAAGATA  
CTTCTGGTTAAGGCCCTCGGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCATCC  
ATCTGGAGGCACAAGGCCCTGGCTGGCTGGAGCTCAGGAGGCCCTGAGGACTGCAACACC  
GGGCCACACCTCTCTGCCCTCCCTGAGTCCTGGGGTGGGAGGATTGAGGGAGCT  
CACTGCCACCTGGCTGGGCTGTCCTGCCACACAGCATGTGCCCTCCCTGAGTGCCTG  
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGGCCACTGGAGTGGGTT  
TTGAGTGGGGAGGCAGGGACAGGGAAAGTAACCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

# FIGURE 100

MHGSCSFLMLLPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCVWGHNKERGRRGLENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVWVAKERIGCGSHFCEKLQGVVEETNIELLVCNYEPPGNVKGRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPGBHVWGPLLGLLLLPPVLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

# FIGURE 101

GTAACTGAGTCAGGCTTTCATTGGAGGCCCCCTAACAGAATTCGGTCATTCTCCAAGTTATGGTGGACGT  
ACTCTCTGTGTTCTCCCTCTGCTGGTTTTCACATTAAGCAGACGGACTTAAGTCACAAACAGAATTATCTTCAT  
CAAGGCAAGTCATGAGGCCACCTTAAAGGCCCTCGAGAAGTGAACAAACARTGAATTGGAGACCACTCC  
AAATCTGGGACCTGAGTCAGGCAAAATTACACTTCTCTCTTGGCTGAAACAGGATTTGAAATACTCCCTGA  
ACATCTGAGAGATTTCTGAGCTTGGAAACTTTGGCTTAGAGCACAACATATTTCAGAGCTCCAACTGATT  
TCCAGCCCTACAGCTCAAAATATCTGTATCTCAACAGCAACCCGACTCACATCAATGGAACTTGGGTATTITGACAA  
TTTGGCCAAACACACTCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAAGATGTTAAACT  
GCCCAACTGCAACATCTGAATTGAACCGAAACAGATTTAAATGATGAGTGGACTGACATTCAAGGCCTTGG  
TGCTCTGAGGACTCTGAAAGAATGGAGTAAAGGAAACTTACAGCTTGGCTGAGCTTGGGCTGAGCAA  
CATGGAAATTGGCAGCTGAGCCATAACACCTAACAGGATTTGGCTTACGGCTGTGCTGAGCT  
GCCAGGAACTTCTCAGGCAACAGGATTCAGCCCTGATGGCTGGGAGTCTGGCAGAAAGCTCAG  
TGAGCTGGACCTAATTCAATCATTATCAAGGTTAGATGATTCAGCAACTTCTGGCTTAAGCTTACTAAATAC  
ACTGACATTTGGAAACACAGACTAGCTACATTGTGATTGTGCTTCCGGGGCTTCCAGTTAAAGACTTT  
GGATCTGAGGACAACTGAAATTCTGGGATTATGGAGATGAATGGTGGAGCTTITGGGCTTGACAAACTGAG  
GGGACTGATACTCAGGAAATCTGGGATCTTCTTACTAAAGGCTTCACTGGTTTGAGATCATTGGAGCA  
TCTAGAGCTGAGTGAACAGGCAATCATGTTTCAAGGAACTTGGCTGGGAGTCTGGCAGAACTT  
GGCTTAAATCATCAAGGCTTGTGGATTGGCAGTCACTGGCAGTAAAGGCTTGGGCTTGGCAGAACTT  
TCAGAGCTTGTGAAATGCGAGTGTGGCCTTACCTCAGCTGCTTAAAGGAGAAGGATTITGGCTTGTAGCCAGA  
TGGCTTGTGTTGTGATGATTITCCCACACCCAGATCACGGTCAAGGAAACACAGTGGGCAATAAAAGGTT  
CAATTGAGATTCTAGCTGCTAGCTGGCAGACTGGGCTTGGCAGACTGGGCTTGGGAAAGACATGA  
ACTACTGATGATGCTGAAATGGAAATTATGCAACCTCAGGGGCAAAAGGGTGGCAGGGTGTGGAGTATACAC  
CATCTTGGCAGGGCTGGCAGGGTGGAAATTCTGCACTGAGGGGAAATATCAGTGTGCTATCCAACTATTGGTT  
ATCCCTACTGTCAAAAGGCAAGTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTC  
CGGAGCTGGGGCAGTGGCAGCTGGAGGAGAGACGGCATGATGTGAGGGAGGATGACGTGTTTATCTG  
TGGGGCAGACAGCTTCCAGCTGAGGGAGAGACGGCATGATGTGAGGGAGGATGACGTGTTTATCTG  
GGAGTGAAGATGAGGACATTGGGTTACAGCTGAGCAGACTGGGCAATAAGGAACTTGGCAGAGTATTTCAGGAAACGTT  
AACTCTGACTGCTCAGAAACACCATCATTTTGGGGCCACTGTGGGAGCCAACTGTGTAACCAAGGGAAACAGC  
CGTCTTCAAGTGTGATGCTGAGGAACTCCCTCCCTTAAACTGACTGAGGAAAGGTGATAGCCATTGGTGGT  
AAACCGAGGGACTTTTGGCAGGGCATCTGGCACTGAGAGGAGGAAACCTGGCCTCAGTGTGATCCCCACTTCAAC  
CTGGGACTGGGGCAGTGGCAGGGCAGTGGCTGGGAGGATGCTGAGGAGGATGCTGAGTACATAGC  
CTGGGTTTGTGTTGTGGGGCAGCTGGCAGTGGCTGGGAGGATGCTGAGGAGGATGACAGGAA  
TTGAGCTTACCATCAACACAGATGAGGAACTTGGCAGAGTATTCTCTGATCTCAGGGAAACGTT  
AGCTGAGCAGGAGGTGGGACTGGTCTCAGAAAGGAAAGGCAACCCAGTGTGTCATCTCAGGGTGG  
ATTTTTCTTACACACATGACAGTGTGGGACCTGCCATTGGACATAGCAGTGAAGCTGATGTGGAGCTG  
CACAGATCTGTTCTTGTGGTTTGGGCTTCAAGGCCCTATGTTGGAAAGGAAATGTGTATGGCTCAGA  
TCTCTTGGAAACATATCATACAGGGTGGCAGTCTGGACTCTGACCAAGGAACTGGGTTAATGGACACTATGGCC  
CATAAAGGAAAGGAGTCTACCCAGTGTCTCATCTTCAAGGAAATCTGGCAACGGAGCTTGGGTTGCTGATCATAGC  
GTGGCTTCACTGTGAGGAAGCTTACACACTAGTTACTCTCAGATCATACACAAAGGGAGGAA  
TTGAGCTTACCATAGACTGAGTGGACCAAGGAAAGCTTACACACTACCTCAACTGAACACTTTT  
AAAGAGAGGAAATCTTGTGTTTAAATGGAGTTGAAATTAAAGGATAAAATGCTTTATATACAGAT  
GAACCAAATTACAAAAGTTATGAAAATTATGAGGAAATCTGAGTGTGATATAAGAATACCTTTAAACTA  
TTTTAACTTGTGTTTATGCAAAAAGTATCTGAAATTAATGATATAATCATGATTTATGTTATGTT  
TTAAATAGAAGTACTTCATTATATTGACACATTATTTAATAAAATGTCATATTGAA

## **FIGURE 102**

## YDLDT

### amino acids 1-10

### Transmembrane domain

amino acids 746-765

#### N-glycosylation sites

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459, 628-632, 669-673, 845-849, 927-931, 939-943, 956-960

#### Glycosaminoglycan attachment site

amino acids 826-830

### Casein kinase II phosphorylation site

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268, 314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653, 671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962, 1013-1017, 1019-1023, 1021-1025

#### Tyrosine kinase phosphorylation site

amino acids 607-615

### N-myristoylation site

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534, 612-618, 623-629, 714-720, 873-879

## FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAATG  
AAGGATG CAGGACGCAGCTTCCTCGAACCGAACCAATGGATAAACCTGATTTGCAAGAGAGAAGGAAC  
GAAGCTTCTCTTGAGGCTTGATCTAACAAATGTGTATTTGTCACACAGGGAGGATTCAAGAATGAAA  
TAACCCAGAGTGGACCCGGGGTTGGTGTCTGACATAAATAATCTTAAGCAGCTGTTCCCTCC  
CCACCCCCAAAAAAAGGATGATTGGAAATGAGAACAGGAGGATTCAAAAGAAAAGATGTTCTTCTC  
TATAAGGAGAAAGTGAGCCAAGGGAGATATTTTGGATGAAAAGTTGGGCTTTTTGACTAAAGTAAAGAACT  
GGTGTTGGTGTCTTCTTGTGAATTCCACAAGAGGAGGAAATTATAATACATCTGCAAGAAA  
TTTCAGAGAAGAAAAGTTGACCCGGCAGATTGAGGATTGAGGATTTGGGGAGAGAACCCAGCAGGCACAGTTGGA  
TTTGTGCTTATGTTGACTAAATTGAGCAGGATAATTGAGTGGGCTTTCATCAACCCACTGGATTTCATGGAATGTTGCT  
GTGATCAGTCTGAATACAACCTGTTGAATTCCAGAGGACCAACACAGGATAATTATGAA**ATGTTGAA**ACAAGAT  
GACCTTACATCCACAGCAGATAATGAGTGGCTTACAGGCTTAAAGGGGGCTTGTGGTGTCTGGCT  
GCTGGCTCTCAACTCTGTGTGCTGGCTGGTCTGGCTGGGGCTCAGACCTGCCCCCTCTGTGTCCTGCAAGAA  
CCAGTTCAGCAAGGTGATTGTGTCGGGAAAAACCTCGCTGAGGTTGGCATCTCCACAAACACAGGCT  
GCTGAACCTCCATGAGAACCAAACTTACAGGATCATCAAACTGAAAGCTTCAAGACTGACTTGGAAATCT  
ACAGTTGAGTAGGAACCATAGAACCACTTGGGATGAAATGGGGCTTCTCATGTGCTGGGCAACCTCAACACTCTGG  
ACTCTTGTGACATCTGTTACTACATCCGGAAATGGGATGTTGATGTTTAAACAGAATTCTTCTGGGCAACTTGG  
GGAAATTGAAACCCATTGAGAACCTCCCTTATGTTTAAACAGAATTCTTCTGGGAAATCA  
CATGTGCAACCTTCCGGAAATCTTCAACCTTCAACCCCTCATAAAATAGATGAGCTGGATCTTCTGGGAAATCA  
TTATGTCCTCATCAGGGCTGGCTTCAACCCCTTCACTGAGGTTGATGACCTGGGGCTTCTGGGCA  
TCAAGTGTGATGGTGAACCGATCTGTTGACACCTTCACTGACTAGTGGAGATCACCTGGCACACA  
ATTACTGCTCATGACCTCTTCACTCCCTGGCATCTAGTGGGACATACATCACAACCCCTGGGA  
TAACACTGTGACATCTGGCTCAGGGTGGTGAATAAGACATGGCCCCCTGAGAACACAGCTGTTGTG  
TAACACTCTCCCAATCTAAAGGGAGGTACATTGGAGAGCTGGCACAGAATTACTTCATGCTATGCTCGGT  
GATTTGAGGAGCCCCCTGAGACCTCAATGACTGAGGCTGAGGCTGAAATGTCGGGCTCCACATC  
CTGACATCTGTATCTGGATTACTCCAAATGGACAGCTGACACATGGGGCTACAAAGTGGGATAGCTG  
GCTCAGTGATGGTACGTTAAATTCAACAAATGTAACCTGCTGAGGATACAGGGATGTACACATGTTGAGTAA  
TTCGGTTGGAAATACTCTGCTCAGGACCCCTGAAATTGTTACTGCTGAGGACCACTACTCTTCT  
AACCCCTCAGACTAGAGACTATGGAACCGTCTAGGATGAGGACGGGACACAGATAACATGTGGTCCACTCC  
AGTGGTCACTGGAGAGACCCCAATGTTGACCCACTCTCAGGATGAGGACGGGACACAGATAACATGTGGTCCACTCC  
CACCATTCCAGTGTGATATAAACAGTGGGATCCAGGAAATTGATGAGGTCTGAGAAGACTACCAAAATCTCAT  
TGGGTGTTCTGGCAGTCAACTCATGCTGAGCTGCTGAGTGTGCAATTCTCAAGATGAGGAAGCAGCACCA  
TCGGCAAAACCATCACGCCAACAGGACTGTGAAATTATAATGTTGAGTGTGAGATTACGGGAGACACACC  
CATGGAAGGCCACTGCCCCATGCTGCTATCGAGCATGAGCAGCTAATCACTATAACTCATACAAATCTCCCT  
CAACCCACACAAACAGTTAACAAATAATTCAATACAGGTTGAGTGTGAGTGTGAGTGGGCTAATCTGAGTCAA  
CTCTAAAGACATGTAACAGAGACTAAAT**TAAACATTCTAGAGTTACAAAACAAACATCAAAAAAA**  
GACAGTTTATTAAGAACACAAATGACTGGGCTAAATTACTGTTCAAAAAGTGTCTTACAAAAAA  
AAAAGAAAAGAAAATTATTATTAACATTTCTATTGATCTGAGTCAAGCAGACAAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTNTRLLNLHENQIQIICKVNSFKHLRHLIELQLSRNHIRTIEGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKDELDSGNHLSAIRPGSFQGLMHQLQKL  
WMIQSQIQVIERNAFDNLQLSVEINLAHNNLTLPHDLFTPLHHLERIHLHHNPWNCDIL  
WLSWWIKDMAPSNTACCACRNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE  
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVNSVGN  
TTASATLNVTAAATTTPFSYFSTVTETMEPSQDEARTTDNNVGPTVVDWETTNVTTSLTPQ  
STRSTEKTFITPVTDINSIGPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIIINVDDITEGDTPMESHLPMPMAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## **FIGURE 105**

## FIGURE 106

MSAPSILRARARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAERPCPTTCRCLGDLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVVLKLNRRNRIASAIPPKMFKLQLQHLELNRKNIKVNVDGLTFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSNMEILQLDHNNLITEITKGWLQYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTFNHLRSRDDSSFLGLSLLNLTIGHGNRVSYIADCAFRLGSSLKTLDLNNEIS  
WTIEDMNGAFSGDLKRLRLILQGNNRIRSIKKAFTGLDALEHLDLSDNAIMSLQGNAFQSMK  
KLQQLHLNTSSLCDCLQKWLPOQVVAENNQFSFVNASCAPQLLKGRSIFAVSPDGFVCDDF  
PKPQTIVQPETOSAIKGSNLSFICSAASSSDPMTFAWKKDNELLHDAEHENYAHLLRAQGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCATAQNSA  
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPQLNWTKDDSPVVTTERHF  
FAAAGNQLLIVDSDVSDAGKYTCEMSNTLGTTERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA  
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETLPADIPSYLSQGTIADRQ  
DGYVSESEGSHHQFVTSSGAGFFLPQHDSGTCIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKGNVYGSDFPETYHTGCSPPRTVLMDHYEPSYIKKKECYPCHPSEESCRSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPESVASSNSFMGTGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLGSGSEEDGKERTDFQEENHICTFKQTLHENYRTPNFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## **FIGURE 107**

## **FIGURE 108**

MEGEEAEQPWFHQPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENFAEEEPVLVLSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRLHRLETLNLQNNRLTSRGLPEKAFFEHTNLNYLYLANNK  
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EVVLILSSNFLRHPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDDLSNNLRSVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPAGLPRRVRTLMILHNQITGIGREDFATTYF  
LEELNLNSYNRITSQPQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIPLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD  
RGRIGKEKEEEEEEEEEEEETR

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## FIGURE 109

GGGGGGGGCTCCGGCGCCGCGACCTGCTCCGGCGCGCCCTCGCCGCTGCTCTCCGGGAGCGGCCAG  
CACTGACCGGGGGCGCGAGGGCTGGGGTTCTCGAGACTCTCAAGAGGGCGCCCTCCATCGCGCCACCAACCC  
CAACCTGTCTCTCGCGCCACTCGCTGCGCCCGCAGGACCCGCTGCCAACATGATTTCTCTGGCGCTGGT  
GCTGGCTATGCTTACCTCGCTACCTCGAGGGCGAGCTGACTCTGTGGGCTGGGCTGCCAGTCTTGGGGAGACTGTCAGCG  
TGGCTATGCTTACCTGGGGAGGATTGACTCTGTGGGCTGGGCTGCCAGTCTTGGGGAGACTGTCAGCG  
TGTGGCAACCCAGATGCAAACACTGGTGAATGTCTGGGCAAAACAGTGCAGAGTGTCACTCGGTTATGCTGG  
AAAAACCTGTAACTCAAGATCTAAATGAGTTGGCTCAAGGCCGGCCCTGTAAGCACAGGTGCAATGAAACACTTA  
CGCGAGCTACAACTGCTACTGTCTCAAGGATATACTGCTATGCGGATGGTCTGCTCAAGTGCCCTGACCTG  
CTCATGGCAAACCTGCTAGTATGGCTGTGATGTTAAAGGACRAATACCGTGCCAGTGCCCATCCTGGGCT  
GCACTGGCTCTGATGGGAGGACCTGTGATGAGTTGAGAATGCTACAGGAAGGCCCTCTGCCCTAGATT  
TAGGGCAATGCTTACACTTTGGAGGACTACCTGCAAGTGTGATGCTCATGTAAGGCTCTGATCTCATGTTATGGAGG  
CAAATATCAATGTCATGACATAGAACGAACTCACTTGTGAGTATGCAAGTGTGAGCTTGAGCAGCTTGTGATGTTATAA  
CTGACTGGCTTACAACTGCAAATGTAAGAAGGATACCAAGGGTGTGACTGACTGTGTTATATCCAAA  
AGTTATGATGAACTTCTCAGGTCCTGAACTTCTGTAAGGAAACTGGTACCATTTAAAGGGTGCACAGGAGAA  
TAATAATTGATCTCTGATGTTGGAGACTTCTGGTGCCTCGAGAACACATATACTCTCTTATCATTTACCA  
CGGGCAACTCTCTAAACACAAACAGGACTACCAAAAGGCCACCAACTTCTACCTCCACCC  
CTGGCCAAACAGAGCTCAGAACACCTTCTACCAACTCACACCCGAAAGGCCAACCCGGACTGACAACATAGC  
ACCCAGCTGCCAACACCTCCAGGGAGGATTACAGTTGACAACAGGTTACAGACAGACCCCTCAGAAACCCAGG  
AGATGTTGCTAGTCTGTCACAGTTGATTTTGACCATGCAATTGTTGGATGGAATCAGGGAGAAGACAA  
TGACTTGCACCTGGAAACCATCTGGGACCCAGCAGGGACAATATCTGACAGTGTGCGGAGCCAAAGCCCCAG  
GGGAAAAGCTGACCGCTGGTCTACCTCTGGCGCCCTGATCGTACCTCAGGGACCTGTGCTGTGTCATCAGGCA  
CAAGGTGAGGGCTGCACTCTGGCAACTCTGGAGGTTGAGAAAACACAGTGTGCCACCGAGCAGGGCTGTG  
GGGAAGAAATGTTGGGCAATGGTGGAGGAAACACAGATCACCTTGCGAGGGCTGACATCAAGAGCAGAACTACA  
AAGAAGATAAAAGGGTTGGAAAAAAAGATCTATGTTGAAAATTAAGGAGACTGGGATTTTGAGCTGGAGAAG  
AGAAGACTGAGGGCAACCAATTGATGGTTTCAAGTATAATGAGGGTGTGACAGAGGGTGGCAAGAGAGGGTGGCAAGCTG  
TTCCTCATATGCACTAAAGAATAGAACAGGAGAAACTGGCTTAGACTAGATATAAGGGAGCATTTCTGGCAGG  
GCCCATTTGTAAGAATACTCTCATAAAAAAAGACTGTGAAAATCTCAGTATCTCTCTCTCTCTCTCTCTCT  
TAAAATTTGCTATTTAAAGATGTTAAAGGATGTTCTTACCCAGGAAAAGTAACAAATTATAGAAATTCCAAA  
AGATTTTGATCTACTAGTAGATGCACTGAAAATCTTAAAGACTTAATTTGAGCTTAATTTAGGCTTAATTAGG  
CATTTCCCTCTGACCTCTTAATGGAGAGGGATTGAAAGGGGAAGAGGCCACCAATGCTGAGCTACTGAAATA  
TCTCTCCCTATGGCAATCTAGACGATTTAAAGAAAAGGAAACTTTATCCAAATGAGAGTATGATGGAC  
AGATATTGATCTCACTAATGTCAGTTGTTGGCTGTGTTCTCATGTTCTCATGTTAAAGGATAAGGCTAAC  
TTTCATTGTTCAATGAGATGTTCTGAGATTTTTTTTAAAGAGATCTTCAAGGAAACAGTTAGAGAG  
ATTTCATGGGTGCTTCTCTGCTGTTGAGCAAGATATCTTGGCTGCTGAGAAAAGAGTGCCCTGGCCC  
ACACGGGAGACCTTCCCTCACCTCATCAGTATGATTCAGTTCTCTTATCAATTGGACTCTCCAGGTTCCAC  
AGAACAGTAATATTGGTAAACAACTAGGTCACATAGAAGGCTTCTCTGCTTAACTCTGGTAAAGGAGGGCTGG  
AGGGGGAAAATAAAATCATTAAGGCTTGTAGTAACGGCAGAAATATGAGCTGAGTCCATTTTAAATGTTCT  
TCCCTTAACTGAGTATAACTGACAGCTGAAGATGAAAGGGAAAATAATGAAATTTTACTTTCTGATGCCAA  
TGATACATGCACTAAACTGATGAGAAGATTCAACAACTACTGTATAACATCTGTTTATTAATTAATGTTT  
CTAAAATAAAATGTTAGTGGTTTCCAAATGGCTAATAAAACAAATTATTTGTAATAAAACACTGTTAGTAAT

## FIGURE 110

MDFLLALVLVSSSLYLQAAAEFDGRWPRQIVSSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP  
RCKHGE CIGPNKCKCHPGYAGKTCNCQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCMANCQYGCDVVKQIRCCPSPGLHLAPDGRTCVDVDECATGRASCFRFRQC  
VNTFGSYICKCHKGFDLMLYIGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPPIHPKGNGTILKGDITGNNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPPLPTPERPTTGLTTIAPAASTPPGGITVDN  
RVQTDPQKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPA GGQYLTVA  
KAARLVLPLGLRMLMHSGDLCLSFRHKVTGLHSGTQLQFVVRKGAHGAALWGRNGGGHWRQTQI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## FIGURE 111

CTTCTTTGAAAAGGATTACACCTGATCAGGTTCTCTGCATTGCCCCCTTAGATGTGA  
AATGTGGCTCAAGGTCTTCAACACTTCCCTTGCACAGGTGCTGCTCGGGCTGA  
AGGTGACAGTGGCATCACACACTGTCCATGGCCTAGAGGTGAGGCCCTACCTACCGTC  
CACTATGGCTTCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCA  
CACATGGCCAAATACTTACTGGCTCTGTGAATAAGCTGTGGTCCCTGACTTGGAAATACC  
AACACAAGTCACCATGATGCCACCCAATGATCTCTGCTTATCAACCCACTGCAGTCCCT  
GATGAAGGCAATTACATCGTAAGGTCAAATTCAAGGGAAATGGAACCTATGCCAGTC  
GAAGATAACAAGTCACGGTTGATGATCTGTCAAAAGCCAGTGGTCAGATTCATCTCCCT  
CTGGGGCTGTGGAGTATGTGGGAAACATGACCTGACATGCCATGTGGAAGGGGGACTCGG  
CTAGCTTACCATGGCTAAAAAATGGAGACCTGTGCCAACACAGCTTACACTCTTTTC  
TCCCCAAACAAATACCCCTCATATTGTCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCCTGGTGGAGGAAACCTGCTAGTGAATAAGGAAATGGAAGTATCATTATGCCCATCATATTAT  
GGACCTTATGGACTTCAGTGAATTCTGATAAAGGGCTAAAGGTAGGGGAAGTGTATTACTGT  
TGACCTGGAGAGGCCATCTTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CTCTGGATTAGGAGGACTGACAACTACATATATCATTAAGCATGGCCTCGCTTAAAGGTT  
GCATCTGAGAAAGTGGAGGAACTCATTTGCAACTTACATGAACTTACATGAAACACATAAC  
CGGCAGGCAAGGATGAAACTCATTCACAGTTATCATCACCTCCGAGACTGGAGAACGTTG  
CACAGAAAGGAAATCATTGCACTTTAGCAAGTATACTGAATATCACTATTTTGATT  
ATATCCATGTGCTCTCTTCTATGGAAAAAAATATACACCTTACAAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAACAGAAATCAGGAAAGGCTTACACATTTCAGGCCATGAAGATG  
CTCTGGATGACTTGGAAATATATGAATTGTTGCTTTCAGATGTTCTGGTGTTCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTTGATCAGGGAAGATTGCAAGTACAGT  
GTATGAAGTTATTAGCAGCACATCCCTGCCAGCAGCAAGGACATCAGAGTGAACCTTCATGG  
GCTAAACAGTACATTGAGTGAATTCTGAAGAAACATTAAAGGAAACAGTGAAAAGT  
ATATTAACTGGAATCAGTGAAGAAACCAGGACCAACACCTTACTCATTATTCTTACA  
TGCAGAAATAGAGGCATTATGCAAAATTGAACTGCAGGTTTTTCAGCATATACAAATGTCCT  
GTGCAACGAAAACATGTTGGGAAATTCTCTCAGTGGAGAGTCCTCTCATGCTGACGG  
GGAGAACGAAAGTGCAGGGTTCTCATAGTTTGTATGAAATATCTCACAAACCTCA  
ATTAGTCTACTCTACACTTCACTATCATCAACACTGAGACTATCTGCTCACCTACAAA  
TGTGGAAACCTTAACTTGTGATTTTCAATTTCAGCAGACTTTGTTTATTAATTTTATAGTG  
TTAAGAATCTAAATTATGTTCAATTTCACAAATTCTATCTGTTATTGTACAA  
CAAAGTAATAAGGATGTTGTCACAAAACAAACTATGCTCTCTTCTTCAATCACC  
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA  
TTTTTCAAGGAAAGATGGATTCAAATAAAATTCTGTTTGCTTTAAAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSAQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMMLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV  
DLGEAILFDPCSADSHPPNTYSWIRRTDNTTYIIKHGPRLLEVASEKVAQKTMGYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

### **FIGURE 113**

## **FIGURE 114**

MAPSGSLAVPLAVLVLLLWGPWTHGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVLMMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQQPYPSKKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIRQRSLGPSSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## FIGURE 115

GGCAGTGTCCAGCTGCGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTTCTGTGTGCCAGAACCGCAAGCAGTTGCTAACCCAGTGGACAGGCGGATTGGAAAGAGCGGGAAAGGCCTGCTGGCTGATGGCTGGTTGGTGTCTGAGCTGTGTGCAAGGCCAATTCTCACCTTATTGGCACATGACTGACCTGATTATGAGAGAAAGAGCTGGCAGTCTCTGAAAGAGTACATCCTTGTGGAGGAAGCCAAGCTTCCAAGATAAGAGCTGGCCAACAAATGGGAAGGCCCTGGACTAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCAACAACTGGCTACAGGACTCAAGCTGCAAGCAGGCTGGAGGACCTTGTCTCTGAGCTGAGGACTCAAGCTGCAAGTGGTATGCCAACACAGACTGGCTGCGCTGGAGGACTTGTCTCTGAGCTGAGGACTCAAGCTGCAAGCTGCCAACGCCCTGAGTGAAGACTTCAGGACACATACAGGGCTGGACCAGGCCAACATTCTCAAGGGGAACCTCAGGAACCAAGTACCGGAATGCTGAGTGTGGATGACTGCTTGGATGGCGCTCGGCTTACATGAGGGACTTATTCATACAGGTGTTGTGGATGGAGCAAGCTGAAAGCAGCTTGTGATGCCGGGGAGGGAGGCCAACACAACAGGACTCACAGGTGCTGGACTACCTCACTATGCTGCTTCCAGTTGGGTGATCTGACCGTGGCTGAGCTCACCCGCCGCTGCTCTCCCTGACCCAAAGGCCAACAGCAGAGCTGGAGGAATCTCGGTACTTTGAGCAGTTATTGGAAGAGAGAGAGAAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAACAGCACTATGAGGGCTGTGACTACCTGGCTAGAGGCTCTGCTGGGAGGGTGTCAACTGACACCCCCTGAGACAGAAGAGGTTTCTGAGGTACCAACATGGCAAACAGGGCCCCACAGCTGCTCATTCAGGCCCCCTAAAGAGGAGGGAGCTGGGACAGCCCCCACAACGGTCAAGGACTACAGTGTCTGATGCTGAGGAAATCGAGAGGATCAAGGAGATCGCAAAACCTAAACTTGCACGAGCCACCGTGTGATCCAAGACAGGAGTCCTACTGTCGCCAGCTACCGGGTTTCCAAAAGCTCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCCGAGTAATCTGCGATGCGACATCACAGGGTTAACAGTAAAGACTGAGCTGGCAGAAATTGTTACAGGGTGTCAAATTTGAGGAGGACAGCTGCTGCTCATTCAGGCGACTCTTGTGACAGCGGCCCTAAACACCTTCTGGGCTGCAATTGCTTAAGAAGGGTACAGCTGTGTTGGTGCACCCGCTCTCCCTGAGCTGGGAGGGTACTACCGAACAGACATGCTGCCCTGCCCTGCTGTGGGCTGCAAGTGGCTCCAAATAAGTGGTTCCATGAACGAGGAGACAGGAGTTCTTGAGACCTTGTGGATAACAGAAGTGTGACTGACATCCCTTTCTGTCCTTCCCTTCTGGTCCTTCAGGCCATGTCAGGCTAACAGTGGGAGAAATGAATGTTGTCTGGACAGAGGAGACCTAACAGGGCGACTCTGTGACTGAAGTCCCAGCCCTTCATTCAAGGCTGTGCCATCCCTGGCCCCAAGGCTAGGATCAAGTGGCTGCAGAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTTTAGGTGTGAGATGTTCTGAGTGAACCAAGTTCTGATACCTTGTGTTACATGTTGTTTATGGCATTCTATCTATTGTGGCTTACCAAAAAATAAAATGTCCCTACCAGAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVVEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAAKALMRLQDTRYLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV  
LWMBQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR  
YFEGQLLEERKTLTNQTEAELATPEGIYERPVDFYLPERDVYESLCRGEVVKLTPRQKRLF  
CRYHHGNRAPQQLIAPFKEEDEWDSPHIVRYYDVMSEDEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS  
RRPFDGSLKT'GNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSSEGDDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 115-119, 264-268

### **Glycosaminoglycan attachment site.**

amino acids 490-494

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

### **Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

### **Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

### **N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

### **Leucine zipper pattern.**

amino acids 213-235

### **FIGURE 117**

## FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD  
QSDEDFKPRIVPYRDPNPKVVLTRYIQTTELGSREFLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGRARAPAGMQVVSQHGDERPAWLMSETLRHLHHTFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSRLLLRLRPHLDGCRG  
DILSARPDEWLGRCLIDSGLGVGCVSQHQGQQYRSFELAKNRDPEKGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAOQIRNLTVLTPGEAGLSWPVGLPAPFTPHSRFEV  
LGWDYFTEQHTFSCADGPKCPLQGASRADVGALETALEQLNRRYQPLRFQKQRLLNGYR  
RDPDARGMEYTL DLLLECVTQRGHRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPLL  
VAEAAAAPAFLEAFANAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKA AAAAELEERRYPG  
TRLAWLAVRAEAPSOVRLMDDVVSKKHPVDTLFFLTWTRGPVEVLNRCRMNAISGWQAFFP  
VHFQEFNPALSPQRSPPGPPGAGPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNAADYLAA  
RARLAGELAGOEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRQLAMALMFEQEQAQNST

### Signal sequence:

amino acids 1-15

### Transmembrane domain:

amino acids 489-507

### N-glycosylation site.

amino acids 121-125, 342-346

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

### Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### Tyrosine kinase phosphorylation site.

amino acids 736-743

### N-myristylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

### Cell attachment sequence.

amino acids 247-250

## **FIGURE 119**

CGGAGTGGTGCGCCAACGTGAGAGGAACCGTGCAGGGCTGCCTTCTGTCCCCAAGCC  
GTTCTAGACGGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTGG  
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAAGAAGATATCTGAAAATTC  
GAGGATGAGCGCATGGAGCTAGTAAGAGCTTGCAGTATACGTATTATCCTGTAAAACC  
CAAAGATGTGAGTCTTGGGCTGAGTAAAGAGACTGGACCAACACTGTGACAAAGCAG  
AGTTCTTCAGTCTGAAAATGTTAAAGTGTGAGTCATTAAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAAATCGCCTTGATAAGTATAGAGACCAATACAACTG  
GTTCTTCCTGACGCCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTAAATCTGGAGACCTGAAATAT  
GTGGGTATGGAAGGAGGAATTGCTTAAGTGTAGAAATCAATGAAAAGACTTAACAGCCTCT  
CAATATCCCAGAAAAGTGTCTGAAACAGGGAGGGATTTGAGAAGATATCTGAGATAAAC  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGAGAAAATGAGATGCTGATGGA  
AAAGATGTATTAAACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAAGGTAGTAGAAGGCTGTTGTCAGATATGGCTGTTACTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGTATGGGTATACCGCCTTAGGGCATTTGGCATATTTCAT  
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTGTATAGGACGTGTTGTCATTGGTAGTAGTAACATACATATCCAA  
TACAGCTGTATGTTCTTTCTTCTAATTGGTGGCACTGGTATAACCACACATTAAG  
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTTAAACACATGAACATTGAAATG  
TGGTGGAAAAGAAGTGTAAAGAATAATAATTGCAAAATAAACTTAAATAATATTAT  
GTGATAAAATTCTAAATTATGAAACATTAGAAATCTGAGGGCACATTTTGCTGATTGGTT  
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAAATGATATCTCTAGTTGTAATT  
TGTGATTAAAGTAAAACCTTGTGTTCCCTTACTCTAAACTGATTATGTTCT  
AAGCCTCCCCAAGTCCAATGGATTGCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA  
ATTAAAGTGAAGTGGAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG  
IVLVSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

### **FIGURE 121**

## **FIGURE 122**

MNSSKSSETQCTERGCFSQMFLLWTVAGIPIFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSCYNYGGSVKNCCPLNWEYFQSSCYFFSTDТИSVALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQVVDGTPLTKSLSFWDVGEPPNNIATLEDATMRDSS  
NPRQNWNNDVTCFLNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## **FIGURE 123**

## FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDMKIQGDLAGRAEILGKTSLIKWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIAASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGINCCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267